SEQUENCE LISTING

<110> Hu, Xu
    Lu, Guihua

<120> Pathogen-Responsive Genes, Promoters,
  Regulatory Elements and Methods of Use for Same

<130> 1469

<150> 60/414,771
<151> 2002-09-30

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aagcacattc gcgcgctgct cgcccgccgc cacggttccg tcaagccgaa cgaagcctcc 180
ataccggagg ccagcgagtg tgagctcggc ctcgacaaga gctttggctt tgctaagcag 240
ttttcggctc attatgagct cagtgacgaa gtcggccggg ggcattttgg gtatacctgc 300
tccgctaaag gcaagaaagg ggcgttcaag ggcttaaatg ttgctgtcaa agtcattcct 360
aaagccaag atg acc aca gca att gct ata gag gat gta agg aga gaa gtg 411
           Met Thr Thr Ala Ile Ala Ile Glu Asp Val Arg Arg Glu Val
            1   5   10

aag ata ttg agg gct tta aca gga cat aag aat ctg gtg caa ttc tat 459
Lys Ile Leu Arg Ala Leu Thr Gly His Lys Asn Leu Val Gln Phe Tyr
 15   20   25   30

gaa gcc tat gaa gat gat gac aat gtt tat ata gtt atg gag ttg tgc 507
Glu Ala Tyr Glu Asp Asp Asp Asn Val Tyr Ile Val Met Glu Leu Cys
                35   40   45

aaa gga ggg gaa ttg cta gat agg att ctt tcc agg ggt gga aag tac 555
Lys Gly Gly Glu Leu Leu Asp Arg Ile Leu Ser Arg Gly Gly Lys Tyr
            50   55   60

tca gaa gag gat gcc aga gta gtt atg atc caa ata ttg agt gtg gta 603
Ser Glu Glu Asp Ala Arg Val Val Met Ile Gln Ile Leu Ser Val Val
            65   70   75

gct ttt tgt cat ctg cag ggt gtt gtt cac cgt gat ctc aag cca gag 651
Ala Phe Cys His Leu Gln Gly Val Val His Arg Asp Leu Lys Pro Glu
    80   85   90

1

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aat ttt ctt ttc act tct aag gat gac aag tcc acg ctg aag gcc att    699
Asn Phe Leu Phe Thr Ser Lys Asp Asp Lys Ser Thr Leu Lys Ala Ile
 95              100              105              110

gat ttt ggg ttg tct gac tat gta aag cca gat gag agg ttg aat gat    747
Asp Phe Gly Leu Ser Asp Tyr Val Lys Pro Asp Glu Arg Leu Asn Asp
             115              120              125

att gtg gga agt gct tat tat gta gct cca gaa gtt ttg cat aga tct    795
Ile Val Gly Ser Ala Tyr Tyr Val Ala Pro Glu Val Leu His Arg Ser
             130              135              140

tat ggg aca gag gca gat atg tgg agc att ggt gta att gct tat att    843
Tyr Gly Thr Glu Ala Asp Met Trp Ser Ile Gly Val Ile Ala Tyr Ile
         145              150              155

ctt tta tgc gga agc cgt ccc ttt tgg gcc cgg aca gaa tct ggt ata    891
Leu Leu Cys Gly Ser Arg Pro Phe Trp Ala Arg Thr Glu Ser Gly Ile
         160              165              170

ttt cgg gct gta ctg aag gca gat cca agt ttt gat gag gct cct tgg    939
Phe Arg Ala Val Leu Lys Ala Asp Pro Ser Phe Asp Glu Ala Pro Trp
175              180              185              190

cct tct tta tcg gtt gat gcc aaa gat ttt gta aag agg ttg ttg aat    987
Pro Ser Leu Ser Val Asp Ala Lys Asp Phe Val Lys Arg Leu Leu Asn
             195              200              205

aag gat tat cgt aaa aga ttg act gcg gct cag gca cta agt cat cca    1035
Lys Asp Tyr Arg Lys Arg Leu Thr Ala Ala Gln Ala Leu Ser His Pro
             210              215              220

tgg ctg gtg aat cat cat gat gat atg agg ata cct ttg gat atg ata    1083
Trp Leu Val Asn His His Asp Asp Met Arg Ile Pro Leu Asp Met Ile
         225              230              235

atc cac aag ctt gtt aaa gct tac att tgc tcg tct tcg ttg cgc aaa    1131
Ile His Lys Leu Val Lys Ala Tyr Ile Cys Ser Ser Ser Leu Arg Lys
         240              245              250

tct gct tta cgg gct ctt gca aag aca tta aca gta gct cag cta gct    1179
Ser Ala Leu Arg Ala Leu Ala Lys Thr Leu Thr Val Ala Gln Leu Ala
255              260              265              270

tat ctc aga gat caa ttt act ctg tta ggg cca aac aaa agt gga tta    1227
Tyr Leu Arg Asp Gln Phe Thr Leu Leu Gly Pro Asn Lys Ser Gly Leu
             275              280              285

att tct atg cag aac ttt aag acg gct gtt ttg agg agc tct aca gat    1275
Ile Ser Met Gln Asn Phe Lys Thr Ala Val Leu Arg Ser Ser Thr Asp
             290              295              300

gcc tca aag gat tca cgg gtc tta gat tat gtc agt atg gtt agt tct    1323
Ala Ser Lys Asp Ser Arg Val Leu Asp Tyr Val Ser Met Val Ser Ser
             305              310              315

atc caa tat agg aaa tta gat ttt gag gag ttt tgt gct gct gct ata    1371
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2

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Ile Gln Tyr Arg Lys Leu Asp Phe Glu Glu Phe Cys Ala Ala Ala Ile
    320                 325                 330

agt gtg cac caa ctc gag gga atg gag acc tgg gag caa cat gca agg   1419
Ser Val His Gln Leu Glu Gly Met Glu Thr Trp Glu Gln His Ala Arg
335                 340                 345                 350

cat gcc tat gag ctt ttt aaa aag gaa gga aat aga cca att atg att   1467
His Ala Tyr Glu Leu Phe Lys Lys Glu Gly Asn Arg Pro Ile Met Ile
                355                 360                 365

gaa gaa ctt gcc tcg gaa ctt ggg ctt agt cca tca gta cct gtt cat   1515
Glu Glu Leu Ala Ser Glu Leu Gly Leu Ser Pro Ser Val Pro Val His
                370                 375                 380

gta gta ctt cag gat tgg ata agg cac tca gat gga aag ctt agt ttc   1563
Val Val Leu Gln Asp Trp Ile Arg His Ser Asp Gly Lys Leu Ser Phe
                385                 390                 395

ttg gga ttt gtc agg ctt ctg cat ggg gtt tct tcc cgc gca ttt cag   1611
Leu Gly Phe Val Arg Leu Leu His Gly Val Ser Ser Arg Ala Phe Gln
    400                 405                 410

aag gct tga gagaatgtac acacagttgc tattattttt tcttgcccgt           1660
Lys Ala  *
415


tacctttaaa tattttgatg gtacctaaat gcatgagcta actccatcag cagacctcag 1720
tgggcttctg caagttgaag gcagtggctg ataggaattt gtttctgaag ctttatgcaa 1780
catatatcta tcccactttt ccaagattta caaacacaac ctatattccc caccttgttt 1840
ctcactcact ttagtttggt ggttctggag ttagaagctt gtacagttga aagctagacc 1900
aaaaattgta cccaccttgt cttaagggtt taccccttgt gtacccatgg cacctatcaa 1960
taaacatcac gtgaactcct tgataataga cagatatgta gccttttttt cgtagtattt 2020
tgttgcattt atatgttatt attattcaag gccacaaggg ttggtacttt ttatatacca 2080
tagcattatt gagttttgaa tctataactt cttgcaaact atgcaaatgc aaaacccttt 2140
tcatcatata tgggtggcat ttggttaatg atctatacac aatatcttta gatggtacca 2200
aacttctaac gatatcagtg taaagttttg cttttgaaga cattcaaaag cttctggagt 2260
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aa                                                                2322

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<212> PRT
<213> Glycine max

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Leu Arg Ala Leu Thr Gly His Lys Asn Leu Val Gln Phe Tyr Glu Ala
            20                  25                  30
Tyr Glu Asp Asp Asp Asn Val Tyr Ile Val Met Glu Leu Cys Lys Gly
        35                  40                  45
Gly Glu Leu Leu Asp Arg Ile Leu Ser Arg Gly Gly Lys Tyr Ser Glu
    50                  55                  60
Glu Asp Ala Arg Val Val Met Ile Gln Ile Leu Ser Val Val Ala Phe
65                  70                  75                  80
Cys His Leu Gln Gly Val Val His Arg Asp Leu Lys Pro Glu Asn Phe
                85                  90                  95
```

3

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Leu Phe Thr Ser Lys Asp Asp Lys Ser Thr Leu Lys Ala Ile Asp Phe
            100                 105                 110
Gly Leu Ser Asp Tyr Val Lys Pro Asp Glu Arg Leu Asn Asp Ile Val
            115                 120                 125
Gly Ser Ala Tyr Tyr Val Ala Pro Glu Val Leu His Arg Ser Tyr Gly
            130                 135                 140
Thr Glu Ala Asp Met Trp Ser Ile Gly Val Ile Ala Tyr Ile Leu Leu
145                 150                 155                 160
Cys Gly Ser Arg Pro Phe Trp Ala Arg Thr Glu Ser Gly Ile Phe Arg
                165                 170                 175
Ala Val Leu Lys Ala Asp Pro Ser Phe Asp Glu Ala Pro Trp Pro Ser
                180                 185                 190
Leu Ser Val Asp Ala Lys Asp Phe Val Lys Arg Leu Leu Asn Lys Asp
            195                 200                 205
Tyr Arg Lys Arg Leu Thr Ala Ala Gln Ala Leu Ser His Pro Trp Leu
    210                 215                 220
Val Asn His His Asp Asp Met Arg Ile Pro Leu Asp Met Ile Ile His
225                 230                 235                 240
Lys Leu Val Lys Ala Tyr Ile Cys Ser Ser Ser Leu Arg Lys Ser Ala
                245                 250                 255
Leu Arg Ala Leu Ala Lys Thr Leu Thr Val Ala Gln Leu Ala Tyr Leu
                260                 265                 270
Arg Asp Gln Phe Thr Leu Leu Gly Pro Asn Lys Ser Gly Leu Ile Ser
            275                 280                 285
Met Gln Asn Phe Lys Thr Ala Val Leu Arg Ser Ser Thr Asp Ala Ser
    290                 295                 300
Lys Asp Ser Arg Val Leu Asp Tyr Val Ser Met Val Ser Ser Ile Gln
305                 310                 315                 320
Tyr Arg Lys Leu Asp Phe Glu Glu Phe Cys Ala Ala Ala Ile Ser Val
                325                 330                 335
His Gln Leu Glu Gly Met Glu Thr Trp Glu Gln His Ala Arg His Ala
            340                 345                 350
Tyr Glu Leu Phe Lys Lys Glu Gly Asn Arg Pro Ile Met Ile Glu Glu
            355                 360                 365
Leu Ala Ser Glu Leu Gly Leu Ser Pro Ser Val Pro Val His Val Val
    370                 375                 380
Leu Gln Asp Trp Ile Arg His Ser Asp Gly Lys Leu Ser Phe Leu Gly
385                 390                 395                 400
Phe Val Arg Leu Leu His Gly Val Ser Ser Arg Ala Phe Gln Lys Ala
            405                 410                 415
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                                             1                   5


ggt gga gag ctt ttc gat agg att att cag cgt ggc cat tat acc gag   103
Gly Gly Glu Leu Phe Asp Arg Ile Ile Gln Arg Gly His Tyr Thr Glu
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4

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aga cag gca gcc aag ctt act aag act ata gtt ggc gtt gtg gaa gct   151
Arg Gln Ala Ala Lys Leu Thr Lys Thr Ile Val Gly Val Val Glu Ala
                25                  30                  35

tgc cat tct ctt ggt gtg atg cac aga gac ctt aaa cct gag aat ttt   199
Cys His Ser Leu Gly Val Met His Arg Asp Leu Lys Pro Glu Asn Phe
        40                  45                  50

ctc ttt gtc aat cag cac gag gat tcc ctt ctc aaa acc att gac ttt   247
Leu Phe Val Asn Gln His Glu Asp Ser Leu Leu Lys Thr Ile Asp Phe
    55                  60                  65

gga tta tct gtc ttc ttt aag cca ggt gat ata ttt aat gat gtg gtg   295
Gly Leu Ser Val Phe Phe Lys Pro Gly Asp Ile Phe Asn Asp Val Val
70                  75                  80                  85

ggc agc cca tac tat gtt gcc ccg gat gtt ttg cga aag cgt tat ggt   343
Gly Ser Pro Tyr Tyr Val Ala Pro Asp Val Leu Arg Lys Arg Tyr Gly
                90                  95                  100

cct gag gca gat gtt tgg agt gct ggt gtt atc ctt tac att ctt ttg   391
Pro Glu Ala Asp Val Trp Ser Ala Gly Val Ile Leu Tyr Ile Leu Leu
            105                 110                 115

agt gga gta cct cca ttt tgg gct gaa aac gaa caa gga ata ttt gaa   439
Ser Gly Val Pro Pro Phe Trp Ala Glu Asn Glu Gln Gly Ile Phe Glu
            120                 125                 130

caa gtt ctg cgt ggt gat ctt gac ttt tct tct gat ccc tgg cct tca   487
Gln Val Leu Arg Gly Asp Leu Asp Phe Ser Ser Asp Pro Trp Pro Ser
        135                 140                 145

att tct gaa agt gca aaa gat tta gta aga aaa atg ctt gtt cgc gac   535
Ile Ser Glu Ser Ala Lys Asp Leu Val Arg Lys Met Leu Val Arg Asp
150                 155                 160                 165

cct aga agg cgg ttg act gca cat caa gta tta tgt cat cct tgg att   583
Pro Arg Arg Arg Leu Thr Ala His Gln Val Leu Cys His Pro Trp Ile
                170                 175                 180

caa gtt gat ggt gta gct cct gac aag cca ctt gat tct gcc gta tta   631
Gln Val Asp Gly Val Ala Pro Asp Lys Pro Leu Asp Ser Ala Val Leu
            185                 190                 195

agt cgc ttg aag caa ttt tct gct atg aac aag ctc aaa aaa atg gcc   679
Ser Arg Leu Lys Gln Phe Ser Ala Met Asn Lys Leu Lys Lys Met Ala
            200                 205                 210

ctt ata att att gca gag agc tta tct gaa gaa gaa ata gct ggc tta   727
Leu Ile Ile Ile Ala Glu Ser Leu Ser Glu Glu Glu Ile Ala Gly Leu
    215                 220                 225

aaa gaa atg ttc aag atg ata gat gca gat aac agt ggt caa atc act   775
Lys Glu Met Phe Lys Met Ile Asp Ala Asp Asn Ser Gly Gln Ile Thr
230                 235                 240                 245
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ttt gaa gaa ctt aaa gct ggt ttg aaa aga gtc ggc gct aat ctt aag    823
Phe Glu Glu Leu Lys Ala Gly Leu Lys Arg Val Gly Ala Asn Leu Lys
             250                 255                 260

gag tct gaa att tat gat tta atg caa gca gct gat gtt gat aac agt    871
Glu Ser Glu Ile Tyr Asp Leu Met Gln Ala Ala Asp Val Asp Asn Ser
         265                 270                 275

ggg aca att gat tac ggc gag ttc ctt gct gca acg ttg cac cgc aac    919
Gly Thr Ile Asp Tyr Gly Glu Phe Leu Ala Ala Thr Leu His Arg Asn
         280                 285                 290

aaa att gaa aga gaa gat aat cta ttt gca gcc ttt tct tac ttt gat    967
Lys Ile Glu Arg Glu Asp Asn Leu Phe Ala Ala Phe Ser Tyr Phe Asp
     295                 300                 305

aaa gat gga agt ggc tat att act cag gaa gaa ctt caa cag gct tgt   1015
Lys Asp Gly Ser Gly Tyr Ile Thr Gln Glu Glu Leu Gln Gln Ala Cys
310                 315                 320                 325

gat gag ttt ggc ata aaa gat gtc cgt ttg gaa gag ata atc aag gaa   1063
Asp Glu Phe Gly Ile Lys Asp Val Arg Leu Glu Glu Ile Ile Lys Glu
             330                 335                 340

att gat gaa gat aat gat gga cgc ata gat tac aat gag ttt gtg gct   1111
Ile Asp Glu Asp Asn Asp Gly Arg Ile Asp Tyr Asn Glu Phe Val Ala
             345                 350                 355

atg atg cag aaa gga aat ctt cca gcg gtt ggt aag aag ggc cta gaa   1159
Met Met Gln Lys Gly Asn Leu Pro Ala Val Gly Lys Lys Gly Leu Glu
             360                 365                 370

aat agc ttc agc gtt aag ttc agg gag gca tta aaa ttg tag          1201
Asn Ser Phe Ser Val Lys Phe Arg Glu Ala Leu Lys Leu *
             375                 380                 385


ttttcattgt catcattgag tttttttttt tttttggtg ctctttatta ccacacatcc 1261
ctccttttca ctttgaaggt tcaagatttt attcatagtg caaagtgttt gcatggggat 1321
atttaggtgg gccttttcat ctctgcagtt attttgtttg cgtccaattt aaaatggatt 1381
tttgtaatta cgagaatata ttaaaaagag atatcttttt ttattattat attaaaaaga 1441
gatatctggt ggagtattac tattagagag gaaatagatt atttgaattg aattgacaca 1501
taaaaaaaaa aaaaaaaaa                                               1520


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<211> 386
<212> PRT
<213> Glycine max


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Met Glu Leu Cys Ala Gly Gly Glu Leu Phe Asp Arg Ile Ile Gln Arg
 1               5                  10                  15
Gly His Tyr Thr Glu Arg Gln Ala Ala Lys Leu Thr Lys Thr Ile Val
             20                  25                  30
Gly Val Val Glu Ala Cys His Ser Leu Gly Val Met His Arg Asp Leu
         35                  40                  45
Lys Pro Glu Asn Phe Leu Phe Val Asn Gln His Glu Asp Ser Leu Leu
     50                  55                  60
Lys Thr Ile Asp Phe Gly Leu Ser Val Phe Phe Lys Pro Gly Asp Ile
```

6

```
         65                          70                          75                          80
Phe Asn Asp Val Val Gly Ser Pro Tyr Tyr Val Ala Pro Asp Val Leu
                         85                          90                          95        .
Arg Lys Arg Tyr Gly Pro Glu Ala Asp Val Trp Ser Ala Gly Val Ile
             100                         105                         110
Leu Tyr Ile Leu Leu Ser Gly Val Pro Pro Phe Trp Ala Glu Asn Glu
             115                         120                         125
Gln Gly Ile Phe Glu Gln Val Leu Arg Gly Asp Leu Asp Phe Ser Ser
             130                         135                         140
Asp Pro Trp Pro Ser Ile Ser Glu Ser Ala Lys Asp Leu Val Arg Lys
145                         150                         155                         160
Met Leu Val Arg Asp Pro Arg Arg Arg Leu Thr Ala His Gln Val Leu
                         165                         170                         175
Cys His Pro Trp Ile Gln Val Asp Gly Val Ala Pro Asp Lys Pro Leu
                         180                         185                         190
Asp Ser Ala Val Leu Ser Arg Leu Lys Gln Phe Ser Ala Met Asn Lys
             195                         200                         205
Leu Lys Lys Met Ala Leu Ile Ile Ile Ala Glu Ser Leu Ser Glu Glu
             210                         215                         220
Glu Ile Ala Gly Leu Lys Glu Met Phe Lys Met Ile Asp Ala Asp Asn
225                         230                         235                         240
Ser Gly Gln Ile Thr Phe Glu Glu Leu Lys Ala Gly Leu Lys Arg Val
                         245                         250                         255
Gly Ala Asn Leu Lys Glu Ser Glu Ile Tyr Asp Leu Met Gln Ala Ala
                         260                         265                         270
Asp Val Asp Asn Ser Gly Thr Ile Asp Tyr Gly Glu Phe Leu Ala Ala
                         275                         280                         285
Thr Leu His Arg Asn Lys Ile Glu Arg Glu Asp Asn Leu Phe Ala Ala
             290                         295                         300
Phe Ser Tyr Phe Asp Lys Asp Gly Ser Gly Tyr Ile Thr Gln Glu Glu
305                         310                         315                         320
Leu Gln Gln Ala Cys Asp Glu Phe Gly Ile Lys Asp Val Arg Leu Glu
                         325                         330                         335
Glu Ile Ile Lys Glu Ile Asp Glu Asp Asn Asp Gly Arg Ile Asp Tyr
                         340                         345                         350
Asn Glu Phe Val Ala Met Met Gln Lys Gly Asn Leu Pro Ala Val Gly
                         355                         360                         365
Lys Lys Gly Leu Glu Asn Ser Phe Ser Val Lys Phe Arg Glu Ala Leu
             370                         375                         380
Lys Leu
385


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<212> DNA
<213> Glycine max

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gaactctgac atgttactct tcctcattct cttgagtgca aagaaattgc tttgaatggg 180
tttttcatgg gatgtrtaga atccccctcc ttcaracact tgtttgatta caatatttgc 240
atatctggaa aatttatagt aaactataat tgttatattt tttgtttaga ggctccgtca 300
cctgatgaaa ttgaagctta tgtggttctg caagaatgcc ttgaaatgag aaaaagatat 360
gtttttagag aagctgttgc tccgtgggat aaagaagtta tatccgaccc cagcacaccc 420
aagcctaacc cagatccatt tttatacatt cctgaaggaa attctgatgt gagttttttt 480
ctcccaccac tgaaaacttg gatctcccta tgttatatgc tgtgattaaa ttagttgtat 540
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7   .

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ttctcttgtg ctacagcatt attttgaaat gcaagatggg gttattcgtg tatatccaga 600
tagagatggt aagtaacagg aatttgttat tgataaactt ggtaatttta tcaccactca 660
aggtgggatc ttatgcatgc ttgcctatta cttgcagcaa aagaagagct ttttcctgta 720
gctgatgcaa ctacatttyt cacygatctt catcacttac ttcgagtcat agcagcaggg 780
aatataagaa ctttatgcca tcataggctc aatcttctag aacaagtaca tctctaattt 840
actgaaacaa actgcagcct atgcttgtat tttaattaca tacaagaatc aattgttgtt 900
tgacaatttc tgtatttttc agaaattcaa tcttcatttg atg             943
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<212> DNA
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<222> (72)...(746)

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tctgaagaag c atg tgt gga ggt gct atc atc tca gac ttc att ggt gtg     110
            Met Cys Gly Gly Ala Ile Ile Ser Asp Phe Ile Gly Val
            1               5                   10

aag cgt ggc cgc aac ctc gcc gcg cag gaa ctg tgg tcc gag ctt gac     158
Lys Arg Gly Arg Asn Leu Ala Ala Gln Glu Leu Trp Ser Glu Leu Asp
  15                  20                  25

cct ttc tct gac ctc ctt ggc ttc gac acc acc acc acc acc acc acc     206
Pro Phe Ser Asp Leu Leu Gly Phe Asp Thr Thr Thr Thr Thr Thr Thr
 30                  35                  40                  45

aac caa cca ccc ctt cca gac aaa aaa gtg gtg tca tca tgt gag aag     254
Asn Gln Pro Pro Leu Pro Asp Lys Lys Val Val Ser Ser Cys Glu Lys
                50                  55                  60

aag aag aag aaa agt gtg agt gca gaa aag aag agt ggt ggg cga gct     302
Lys Lys Lys Lys Ser Val Ser Ala Glu Lys Lys Ser Gly Gly Arg Ala
                65                  70                  75

cgg aag aac gtg tac aga gga atc agg caa agg ccg tgg ggc aag tgg     350
Arg Lys Asn Val Tyr Arg Gly Ile Arg Gln Arg Pro Trp Gly Lys Trp
        80                  85                  90

gcc gcg gaa ata agg gac cca cat aag ggc gtc cgc gtc tgg ctc ggc     398
Ala Ala Glu Ile Arg Asp Pro His Lys Gly Val Arg Val Trp Leu Gly
    95                  100                 105

acc ttc ccc acc gcc gag gaa gcc gcc cga gcc tac gac gac gcc gcc     446
Thr Phe Pro Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Asp Ala Ala
110                 115                 120                 125

aag cgc atc cgc ggc gac aag gcc aag ctc aac ttc ccg gcc acc gct     494
Lys Arg Ile Arg Gly Asp Lys Ala Lys Leu Asn Phe Pro Ala Thr Ala
                130                 135                 140

ccg cca ccc tcc aaa aaa caa cgc tgc ctc agc cct gac acc acc acc     542
Pro Pro Pro Ser Lys Lys Gln Arg Cys Leu Ser Pro Asp Thr Thr Thr
                145                 150                 155
```
8

```
gaa caa agc agc agc tca caa tcc acc act gga tcc acc gga tcg ccg    590
Glu Gln Ser Ser Ser Ser Gln Ser Thr Thr Gly Ser Thr Gly Ser Pro
            160             165             170

cct tcc gcc gcc ttc cac ggc gga gga gat gaa ctc gac ctg aaa caa    638
Pro Ser Ala Ala Phe His Gly Gly Gly Asp Glu Leu Asp Leu Lys Gln
        175             180             185

ctt gaa cgg ttt cta ggg ttg gac aac atg ggt gct gag tgg gac aac    686
Leu Glu Arg Phe Leu Gly Leu Asp Asn Met Gly Ala Glu Trp Asp Asn
190             195             200             205

atg gat gac ctg tgg atg ctg gac gac gtc gtt gtg ccc aac cgt cac    734
Met Asp Asp Leu Trp Met Leu Asp Asp Val Val Val Pro Asn Arg His
            210             215             220

tta att tac tag aagggagata attaattaat taataaatgg cgttttctta        786
Leu Ile Tyr  *


agttatagtt ttataaaact atgttggtgt atgtgttctt agttttctgt tttgtcttgt 846
cctctcgctt tggtaatttc tgttttgtac ggtcgaatga tttcaaaatt atgtgcaacg 906
tatcatgaga gggatgatta tatgttatga ttatgattat aaataaaggc caattagggt 966
gtgttaaaaa aaaaaaaaaa aaa                                          989
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<211> 224
<212> PRT
<213> Glycine max

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Met Cys Gly Gly Ala Ile Ile Ser Asp Phe Ile Gly Val Lys Arg Gly
 1               5                  10                  15
Arg Asn Leu Ala Ala Gln Glu Leu Trp Ser Glu Leu Asp Pro Phe Ser
            20                  25                  30
Asp Leu Leu Gly Phe Asp Thr Thr Thr Thr Thr Thr Asn Gln Pro
        35                  40                  45
Pro Leu Pro Asp Lys Lys Val Val Ser Ser Cys Glu Lys Lys Lys Lys
        50                  55                  60
Lys Ser Val Ser Ala Glu Lys Lys Ser Gly Gly Arg Ala Arg Lys Asn
65                  70                  75                  80
Val Tyr Arg Gly Ile Arg Gln Arg Pro Trp Gly Lys Trp Ala Ala Glu
                85                  90                  95
Ile Arg Asp Pro His Lys Gly Val Arg Val Trp Leu Gly Thr Phe Pro
            100             105             110
Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Asp Ala Ala Lys Arg Ile
        115             120             125
Arg Gly Asp Lys Ala Lys Leu Asn Phe Pro Ala Thr Ala Pro Pro Pro
        130             135             140
Ser Lys Lys Gln Arg Cys Leu Ser Pro Asp Thr Thr Thr Glu Gln Ser
145             150             155             160
Ser Ser Ser Gln Ser Thr Thr Gly Ser Thr Gly Ser Pro Pro Ser Ala
            165             170             175
Ala Phe His Gly Gly Gly Asp Glu Leu Asp Leu Lys Gln Leu Glu Arg
            180             185             190
Phe Leu Gly Leu Asp Asn Met Gly Ala Glu Trp Asp Asn Met Asp Asp
        195             200             205
```

9

```
Leu Trp Met Leu Asp Asp Val Val Val Pro Asn Arg His Leu Ile Tyr
    210                 215                 220


<210> 8
<211> 969
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (49)...(762)

<400> 8
agtaactctc tatttctctt tccatctctc aagttctgaa gaagaaac atg tgt gga    57
                                                      Met Cys Gly
                                                        1


ggt gct atc atc tca gac ttc att ggt gtg aag cgt ggc cgc aac ctc   105
Gly Ala Ile Ile Ser Asp Phe Ile Gly Val Lys Arg Gly Arg Asn Leu
      5                  10                  15

gcc gcg cag gaa cta tgg tct gag ctt gac cct ttc tct gac ttc ctt   153
Ala Ala Gln Glu Leu Trp Ser Glu Leu Asp Pro Phe Ser Asp Phe Leu
 20                  25                  30                  35

ggc ttc gat acc acc aat tcc aaa aac caa cca ccc ctg cag aaa att   201
Gly Phe Asp Thr Thr Asn Ser Lys Asn Gln Pro Pro Leu Gln Lys Ile
                40                  45                  50

cca gac aaa aaa gtg gtg tca tca tgt gag aag aag aag aaa agc gtg   249
Pro Asp Lys Lys Val Val Ser Ser Cys Glu Lys Lys Lys Lys Ser Val
            55                  60                  65

gtg ggt gca gaa aag aag aag agt gat agt ggg cga gct cgt aaa aac   297
Val Gly Ala Glu Lys Lys Lys Ser Asp Ser Gly Arg Ala Arg Lys Asn
            70                  75                  80

gtg tac aga gga atc agg caa agg cca tgg ggc aag tgg gcc gcg gag   345
Val Tyr Arg Gly Ile Arg Gln Arg Pro Trp Gly Lys Trp Ala Ala Glu
        85                  90                  95

ata agg gac cca cac aag ggt gtt cgt gtc tgg ctc ggc acc ttc ccc   393
Ile Arg Asp Pro His Lys Gly Val Arg Val Trp Leu Gly Thr Phe Pro
100                 105                 110                 115

acc gcc gaa gaa gcc gcc caa gcc tac gac gac gcc gcc ata cgc atc   441
Thr Ala Glu Glu Ala Ala Gln Ala Tyr Asp Asp Ala Ala Ile Arg Ile
                120                 125                 130

cgc ggc gac aag gcc aag ctc aac ttc ccg gcc acc acc att tcc gcc   489
Arg Gly Asp Lys Ala Lys Leu Asn Phe Pro Ala Thr Thr Ile Ser Ala
                135                 140                 145

gcc gcc gct ccg cca cct tcc aaa aag caa cgc tgc ctc agc cct gac   537
Ala Ala Ala Pro Pro Pro Ser Lys Lys Gln Arg Cys Leu Ser Pro Asp
            150                 155                 160
```

10

```
atc atc act gaa gaa agc agc agc agc agc tca cat tcc acc act gga    585
Ile Ile Thr Glu Glu Ser Ser Ser Ser Ser Ser His Ser Thr Thr Gly
    165                 170                 175

tcc acc ggc gaa agc ggc gga gga aac gac gaa ctc gac ctg aaa caa    633
Ser Thr Gly Glu Ser Gly Gly Gly Asn Asp Glu Leu Asp Leu Lys Gln
180                 185                 190                 195

att gaa tgg ttt cta ggt ttg gag aat gag ctg cct gtt agc aac aac    681
Ile Glu Trp Phe Leu Gly Leu Glu Asn Glu Leu Pro Val Ser Asn Asn
                200                 205                 210

att ggt gct gag tgg gac aac atg gat gac ctg tgg atg ctg gac gac    729
Ile Gly Ala Glu Trp Asp Asn Met Asp Asp Leu Trp Met Leu Asp Asp
                215                 220                 225

gtc gtt gtg ccc aac cgt cac tta att tac tag aaggctaata attaataaat 782
Val Val Val Pro Asn Arg His Leu Ile Tyr  *
                230                 235

ggcgttttct taagttttag ttttacttta taaattgtag tataaaacta tgttggtatt 842
tgtgttctta gtttcttct gctgttttgt ctcttctctg gctttggtaa tttctgtttt 902
ggacggttga atgatttcaa aattaggtac ttaattacac cctatcaaaa aaaaaaaaa 962
aaaaaaa                                                             969
```

<210> 9
<211> 237
<212> PRT
<213> Glycine max

<400> 9
```
Met Cys Gly Gly Ala Ile Ile Ser Asp Phe Ile Gly Val Lys Arg Gly
 1               5                   10                  15
Arg Asn Leu Ala Ala Gln Glu Leu Trp Ser Glu Leu Asp Pro Phe Ser
                20                  25                  30
Asp Phe Leu Gly Phe Asp Thr Thr Asn Ser Lys Asn Gln Pro Pro Leu
            35                  40                  45
Gln Lys Ile Pro Asp Lys Lys Val Val Ser Ser Cys Glu Lys Lys Lys
        50                  55                  60
Lys Ser Val Val Gly Ala Glu Lys Lys Lys Ser Asp Ser Gly Arg Ala
65                  70                  75                  80
Arg Lys Asn Val Tyr Arg Gly Ile Arg Gln Arg Pro Trp Gly Lys Trp
                85                  90                  95
Ala Ala Glu Ile Arg Asp Pro His Lys Gly Val Arg Val Trp Leu Gly
            100                 105                 110
Thr Phe Pro Thr Ala Glu Glu Ala Ala Gln Ala Tyr Asp Asp Ala Ala
            115                 120                 125
Ile Arg Ile Arg Gly Asp Lys Ala Lys Leu Asn Phe Pro Ala Thr Thr
    130                 135                 140
Ile Ser Ala Ala Ala Ala Pro Pro Pro Ser Lys Lys Gln Arg Cys Leu
145                 150                 155                 160
Ser Pro Asp Ile Ile Thr Glu Glu Ser Ser Ser Ser Ser His Ser
                165                 170                 175
Thr Thr Gly Ser Thr Gly Glu Ser Gly Gly Gly Asn Asp Glu Leu Asp
            180                 185                 190
Leu Lys Gln Ile Glu Trp Phe Leu Gly Leu Glu Asn Glu Leu Pro Val
        195                 200                 205
Ser Asn Asn Ile Gly Ala Glu Trp Asp Asn Met Asp Asp Leu Trp Met
```
11

```
        210                     215                     220
Leu Asp Asp Val Val Val Pro Asn Arg His Leu Ile Tyr
225                     230                     235


<210> 10
<211> 856
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (111)...(719)

<400> 10
gtggcggccg ctctagaact agtggatccc ccgggctgca ggaattcggc acgagcacac 60
attggtgttt ccaccaaata cagtgagcaa agttagctga aaattaaaac atg gtt     116
                                                          Met Val
                                                           1


tcc gcc acc gtg gat tcc gat ttt gca ttc ttg gaa tct gtt caa caa  164
Ser Ala Thr Val Asp Ser Asp Phe Ala Phe Leu Glu Ser Val Gln Gln
          5                  10                  15


tac cta ctt gga cat gat tcc atc aat ctc atg tct gaa acc cac caa  212
Tyr Leu Leu Gly His Asp Ser Ile Asn Leu Met Ser Glu Thr His Gln
         20                  25                  30


gct gca tct cat gat cca ttt tca gac cct aat aaa tgt gat ggt gat  260
Ala Ala Ser His Asp Pro Phe Ser Asp Pro Asn Lys Cys Asp Gly Asp
 35                  40                  45                  50


tca ggg aac att gct ttc cga agt gag gat gca acg gct gtg gta gcg  308
Ser Gly Asn Ile Ala Phe Arg Ser Glu Asp Ala Thr Ala Val Val Ala
                  55                  60                  65


cgt gat cat gcg cca cca aca tgg aag cat tac aga ggg gtg agg cgt  356
Arg Asp His Ala Pro Pro Thr Trp Lys His Tyr Arg Gly Val Arg Arg
                  70                  75                  80


aga ccg tgg gga aag ttt gcg gcc gag att agg gat cca aag aag aac  404
Arg Pro Trp Gly Lys Phe Ala Ala Glu Ile Arg Asp Pro Lys Lys Asn
                  85                  90                  95


gga gct agg gtt tgg ctt ggc acg tat gat acc gaa gag aag gcc gct  452
Gly Ala Arg Val Trp Leu Gly Thr Tyr Asp Thr Glu Glu Lys Ala Ala
         100                 105                 110


ttg gca tat gac aaa gcc gct ttc aaa atg cga ggc caa aag gcc aag  500
Leu Ala Tyr Asp Lys Ala Ala Phe Lys Met Arg Gly Gln Lys Ala Lys
115                 120                 125                 130


ctg aat ttt cct cat ctt att gat tcc gac aat tcc gat gaa ttg tcg  548
Leu Asn Phe Pro His Leu Ile Asp Ser Asp Asn Ser Asp Glu Leu Ser
                  135                 140                 145


gag cca gta atg atg aca act tcc aag cga agt ttg tta gaa att tca  596
Glu Pro Val Met Met Thr Thr Ser Lys Arg Ser Leu Leu Glu Ile Ser
```

12

```
tca ccg tcg tcc tcg tgt tca gat gat agc tca gaa tca caa ggg aca   644
Ser Pro Ser Ser Ser Cys Ser Asp Asp Ser Ser Glu Ser Gln Gly Thr
        165                 170                 175

aag agg agg aag agc ctg gct gaa cta ctg aat aaa tta gcc aag aat   692
Lys Arg Arg Lys Ser Leu Ala Glu Leu Leu Asn Lys Leu Ala Lys Asn
    180                 185                 190

aga agc caa gtc aag gtg gaa tgt tga agtggctaga ggaatatgca         739
Arg Ser Gln Val Lys Val Glu Cys  *
195                 200

tgttgtacaa tttgatcaat cattaatatg agacttcaac gattgtaatg taatctggtg 799
ttcatagaat taatgcaatt ttgttcacca aaaaaaaaaa aaaaaaaaaa aaaaaaa    856
```

<210> 11
<211> 202
<212> PRT
<213> Glycine max

<400> 11
```
Met Val Ser Ala Thr Val Asp Ser Asp Phe Ala Phe Leu Glu Ser Val
 1               5                   10                  15
Gln Gln Tyr Leu Leu Gly His Asp Ser Ile Asn Leu Met Ser Glu Thr
            20                  25                  30
His Gln Ala Ala Ser His Asp Pro Phe Ser Asp Pro Asn Lys Cys Asp
        35                  40                  45
Gly Asp Ser Gly Asn Ile Ala Phe Arg Ser Glu Asp Ala Thr Ala Val
    50                  55                  60
Val Ala Arg Asp His Ala Pro Pro Thr Trp Lys His Tyr Arg Gly Val
65                  70                  75                  80
Arg Arg Arg Pro Trp Gly Lys Phe Ala Ala Glu Ile Arg Asp Pro Lys
            85                  90                  95
Lys Asn Gly Ala Arg Val Trp Leu Gly Thr Tyr Asp Thr Glu Glu Lys
            100                 105                 110
Ala Ala Leu Ala Tyr Asp Lys Ala Ala Phe Lys Met Arg Gly Gln Lys
            115                 120                 125
Ala Lys Leu Asn Phe Pro His Leu Ile Asp Ser Asp Asn Ser Asp Glu
            130                 135                 140
Leu Ser Glu Pro Val Met Met Thr Thr Ser Lys Arg Ser Leu Leu Glu
145                 150                 155                 160
Ile Ser Ser Pro Ser Ser Ser Cys Ser Asp Asp Ser Ser Glu Ser Gln
                165                 170                 175
Gly Thr Lys Arg Arg Lys Ser Leu Ala Glu Leu Leu Asn Lys Leu Ala
            180                 185                 190
Lys Asn Arg Ser Gln Val Lys Val Glu Cys
            195                 200
```

<210> 12
<211> 854
<212> DNA
<213> Glycine max

<220>
<221> CDS

13

<222> (115)...(723)

<400> 12

```
aagctggagc tccaccgcgg tggcggccgc tctagaacta gtggatcccc cgggctgcag 60
gaattcggca cgagccacca aatacagtga gcaaagttag ctgaaaatta aaac atg   117
                                                                Met
                                                                1
```

```
gtt tcc gcc acc gtg gat tcc gat ttt gca ttc ttg gaa tct gtt caa   165
Val Ser Ala Thr Val Asp Ser Asp Phe Ala Phe Leu Glu Ser Val Gln
            5                   10                  15
```

```
caa tac cta ctt gga cat gat tcc atc aat ctc atg tct gaa acc cac   213
Gln Tyr Leu Leu Gly His Asp Ser Ile Asn Leu Met Ser Glu Thr His
            20                  25                  30
```

```
caa gct gca tct cat gat cca ttt tca gac cct aat aaa tgt gat ggt   261
Gln Ala Ala Ser His Asp Pro Phe Ser Asp Pro Asn Lys Cys Asp Gly
        35                  40                  45
```

```
gat tca ggg aac att gct ttc cga agt gag gat gca acg gct gtg gtg   309
Asp Ser Gly Asn Ile Ala Phe Arg Ser Glu Asp Ala Thr Ala Val Val
 50                  55                  60                  65
```

```
gct cgt gat cat gcg cca caa aca tgg aag cat tac aga ggg gtg aga   357
Ala Arg Asp His Ala Pro Gln Thr Trp Lys His Tyr Arg Gly Val Arg
                70                  75                  80
```

```
cgt aga ccg tgg gga aag ttt gcg gcc gag att agg gat cca aag aag   405
Arg Arg Pro Trp Gly Lys Phe Ala Ala Glu Ile Arg Asp Pro Lys Lys
                85                  90                  95
```

```
aac gga gct agg gtt tgg ctt ggc acg tat gat acc gaa gag aag gcg   453
Asn Gly Ala Arg Val Trp Leu Gly Thr Tyr Asp Thr Glu Glu Lys Ala
            100                 105                 110
```

```
gct ttg gca tat gac aaa gcc gct ttc aaa atg cga ggc caa aag gcc   501
Ala Leu Ala Tyr Asp Lys Ala Ala Phe Lys Met Arg Gly Gln Lys Ala
        115                 120                 125
```

```
aag ctg aat ttt cct cat ctt att gat tcc gac aat tcc gat gaa ttg   549
Lys Leu Asn Phe Pro His Leu Ile Asp Ser Asp Asn Ser Asp Glu Leu
130                 135                 140                 145
```

```
tcg gag cca gta atg atg aca act tcc aag cga agt ttg tta gaa att   597
Ser Glu Pro Val Met Met Thr Thr Ser Lys Arg Ser Leu Leu Glu Ile
                150                 155                 160
```

```
tca tca ccg tcg tcc tcg tat tca gat gat agc tca gaa tca caa ggg   645
Ser Ser Pro Ser Ser Ser Tyr Ser Asp Asp Ser Ser Glu Ser Gln Gly
                165                 170                 175
```

```
aca aag agg agg aag agc ctt gct gaa cta ctg aat aaa tta gcc aag   693
Thr Lys Arg Arg Lys Ser Leu Ala Glu Leu Leu Asn Lys Leu Ala Lys
            180                 185                 190
```

```
aat aga agc caa gtc aag gtg gaa tgt tga agtggctaga tgaatatgca     743
Asn Arg Ser Gln Val Lys Val Glu Cys  *
```

14

tgttgtacaa tttgatcaat cattaatatg agacttcaac gattgtaatg taatctggtg 803
ttcatagaat taatgcaatt ttgttcacca taaaaaaaaa aaaaaaaaa a   854

<210> 13
<211> 202
<212> PRT
<213> Glycine max

<400> 13

```
Met Val Ser Ala Thr Val Asp Ser Asp Phe Ala Phe Leu Glu Ser Val
1               5                   10                  15
Gln Gln Tyr Leu Leu Gly His Asp Ser Ile Asn Leu Met Ser Glu Thr
            20                  25                  30
His Gln Ala Ala Ser His Asp Pro Phe Ser Asp Pro Asn Lys Cys Asp
        35                  40                  45
Gly Asp Ser Gly Asn Ile Ala Phe Arg Ser Glu Asp Ala Thr Ala Val
        50                  55                  60
Val Ala Arg Asp His Ala Pro Gln Thr Trp Lys His Tyr Arg Gly Val
65                  70                  75                  80
Arg Arg Arg Pro Trp Gly Lys Phe Ala Ala Glu Ile Arg Asp Pro Lys
            85                  90                  95
Lys Asn Gly Ala Arg Val Trp Leu Gly Thr Tyr Asp Thr Glu Glu Lys
            100                 105                 110
Ala Ala Leu Ala Tyr Asp Lys Ala Ala Phe Lys Met Arg Gly Gln Lys
            115                 120                 125
Ala Lys Leu Asn Phe Pro His Leu Ile Asp Ser Asp Asn Ser Asp Glu
        130                 135                 140
Leu Ser Glu Pro Val Met Met Thr Thr Ser Lys Arg Ser Leu Leu Glu
145                 150                 155                 160
Ile Ser Ser Pro Ser Ser Ser Tyr Ser Asp Asp Ser Ser Glu Ser Gln
            165                 170                 175
Gly Thr Lys Arg Arg Lys Ser Leu Ala Glu Leu Leu Asn Lys Leu Ala
            180                 185                 190
Lys Asn Arg Ser Gln Val Lys Val Glu Cys
            195                 200
```

<210> 14
<211> 858
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (7)...(648)

<400> 14

```
aaaaca atg aag acc aaa ctg cta gca ttt ctc ctc ttc ttt gcc ttg      48
       Met Lys Thr Lys Leu Leu Ala Phe Leu Leu Phe Phe Ala Leu
        1           5                   10

act aca aaa cca cta cta ctt gga gca gct gga gct gct cca gag cca      96
Thr Thr Lys Pro Leu Leu Leu Gly Ala Ala Gly Ala Ala Pro Glu Pro
 15                 20                  25                  30

gtg att gat aca tca ggc aag aag ctg aga gct gat gca aat tac cat      144
```

```
Val Ile Asp Thr Ser Gly Lys Lys Leu Arg Ala Asp Ala Asn Tyr His
                35                  40                  45

atc atc cct gca gtg ccc ttc acc ata tgt ggc ttt gtt agc tgt ttc    192
Ile Ile Pro Ala Val Pro Phe Thr Ile Cys Gly Phe Val Ser Cys Phe
            50                  55                  60

act ggt gga ggc ctt tca cta gac agc ata gat gaa tct tgc cct ctt    240
Thr Gly Gly Gly Leu Ser Leu Asp Ser Ile Asp Glu Ser Cys Pro Leu
            65                  70                  75

gat gta ata att gag aaa gcc aat gaa ggc cta cca ctg aga ttc tca    288
Asp Val Ile Ile Glu Lys Ala Asn Glu Gly Leu Pro Leu Arg Phe Ser
        80                  85                  90

cca gtt aac acc aaa aaa ggt gtt att cgt gtc tcc acc gat ttg aac    336
Pro Val Asn Thr Lys Lys Gly Val Ile Arg Val Ser Thr Asp Leu Asn
 95                  100                 105                 110

att ttt ttc tct gat tct gat gaa agg tgt cca cac cat tcc act gtg    384
Ile Phe Phe Ser Asp Ser Asp Glu Arg Cys Pro His His Ser Thr Val
                115                 120                 125

tgg atg ctt gat caa ttt gat gcc tct att gga cag aca tat gtg acc    432
Trp Met Leu Asp Gln Phe Asp Ala Ser Ile Gly Gln Thr Tyr Val Thr
                130                 135                 140

act ggt ggt gtt gtt gga aac ccg ggt gag cac aca att ctg aat tgg    480
Thr Gly Gly Val Val Gly Asn Pro Gly Glu His Thr Ile Leu Asn Trp
            145                 150                 155

ttc aag att cag aag tat gag gat gct tat aag ctg gtc tat tgc cct    528
Phe Lys Ile Gln Lys Tyr Glu Asp Ala Tyr Lys Leu Val Tyr Cys Pro
        160                 165                 170

agg gtg tgc ccc tct tgc cac cat ctg tgc aag gat att gga atg ttt    576
Arg Val Cys Pro Ser Cys His His Leu Cys Lys Asp Ile Gly Met Phe
175                 180                 185                 190

gtg gat gcc aat agg aga atg cat ctg gct ctc agt gat gat ccc ttc    624
Val Asp Ala Asn Arg Arg Met His Leu Ala Leu Ser Asp Asp Pro Phe
                195                 200                 205

aaa att aag ttc aaa gaa gcc tga gatcaaagct ctttcaaatg atggcaaaat    678
Lys Ile Lys Phe Lys Glu Ala  *
                210


taaatgacaa tccatgaata cgtgtgttta taatgatcga tccttgaaat tatatttctt 738
tgtgaagaat tagtaaatga ataaaaaaat taagagtgta tgtttttgtc ctgctgttac 798
aactttaatt tcactattaa ataataaata caattttaa taaaaaaaaa aaaaaaaaaa 858


<210> 15
<211> 213
<212> PRT
<213> Glycine max

<400> 15
```

16

```
Met Lys Thr Lys Leu Leu Ala Phe Leu Leu Phe Phe Ala Leu Thr Thr
1               5                   10                  15
Lys Pro Leu Leu Leu Gly Ala Ala Gly Ala Ala Pro Glu Pro Val Ile
            20                  25                  30
Asp Thr Ser Gly Lys Lys Leu Arg Ala Asp Ala Asn Tyr His Ile Ile
            35                  40                  45
Pro Ala Val Pro Phe Thr Ile Cys Gly Phe Val Ser Cys Phe Thr Gly
    50·                  55                  60
Gly Gly Leu Ser Leu Asp Ser Ile Asp Glu Ser Cys Pro Leu Asp Val
65                  70                  75                  80
Ile Ile Glu Lys Ala Asn Glu Gly Leu Pro Leu Arg Phe Ser Pro Val
                85                  90                  95
Asn Thr Lys Lys Gly Val Ile Arg Val Ser Thr Asp Leu Asn Ile Phe
            100                 105                 110
Phe Ser Asp Ser Asp Glu Arg Cys Pro His His Ser Thr Val Trp Met
            115                 120                 125
Leu Asp Gln Phe Asp Ala Ser Ile Gly Gln Thr Tyr Val Thr Thr Gly
    130                 135                 140
Gly Val Val Gly Asn Pro Gly Glu His Thr Ile Leu Asn Trp Phe Lys
145                 150                 155                 160
Ile Gln Lys Tyr Glu Asp Ala Tyr Lys Leu Val Tyr Cys Pro Arg Val
            165                 170                 175
Cys Pro Ser Cys His His Leu Cys Lys Asp Ile Gly Met Phe Val Asp
            180                 185                 190
Ala Asn Arg Arg Met His Leu Ala Leu Ser Asp Asp Pro Phe Lys Ile
            195                 200                 205
Lys Phe Lys Glu Ala
    210


<210> 16
<211> 846
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (33)...(662)

<400> 16
cacaaactaa ttaaccaaaa gcatacaaaa ca atg aag agc aca atg ctg cta    53
                                    Met Lys Ser Thr Met Leu Leu
                                    1               5


gca ttt gcc ctt gtc tta gcc ttg agt tca caa cca ctg cta gga gga    101
Ala Phe Ala Leu Val Leu Ala Leu Ser Ser Gln Pro Leu Leu Gly Gly
        10                  15                  20

gct gaa gcc tca ccc gag caa gtg gtt gac aca tta ggc aag aag ctc    149
Ala Glu Ala Ser Pro Glu Gln Val Val Asp Thr Leu Gly Lys Lys Leu
        25                  30                  35

cga gtt gga acc aat tac tat att gtc cca tct ctt ccc tac acc aaa    197
Arg Val Gly Thr Asn Tyr Tyr Ile Val Pro Ser Leu Pro Tyr Thr Lys
40                  45                  50                  55

att aga acc act aga ggc ctt ggc cta gcc agt gtt gga aaa cct tat    245
Ile Arg Thr Thr Arg Gly Leu Gly Leu Ala Ser Val Gly Lys Pro Tyr
```
17

```
tgt cct ctt gat gtt gtg gtt gtg aat gga tac cat ggc ttg cca gtg   293
Cys Pro Leu Asp Val Val Val Val Asn Gly Tyr His Gly Leu Pro Val
            75                  80                  85

aca ttc tca cca gtt aat cct aag aaa ggg gtc att cgt gtc tca act   341
Thr Phe Ser Pro Val Asn Pro Lys Lys Gly Val Ile Arg Val Ser Thr
        90                  95                  100

gat ttg aac atc aag ttc tct gct cgc act agt tgt ccc cgc caa tat   389
Asp Leu Asn Ile Lys Phe Ser Ala Arg Thr Ser Cys Pro Arg Gln Tyr
    105                 110                 115

tcc acg gtt tgg aaa ctt gat gat ttt gat ttc tca aag aga caa tgg   437
Ser Thr Val Trp Lys Leu Asp Asp Phe Asp Phe Ser Lys Arg Gln Trp
120                 125                 130                 135

ttt gtg acc act ggt ggt gtt gtg gga aac cct agc ttg gaa acc atc   485
Phe Val Thr Thr Gly Gly Val Val Gly Asn Pro Ser Leu Glu Thr Ile
                140                 145                 150

cac aac tgg ttc aag att gag aag tac gat ggt gct tac aaa ttg gtc   533
His Asn Trp Phe Lys Ile Glu Lys Tyr Asp Gly Ala Tyr Lys Leu Val
                155                 160                 165

tat tgt ccc agc gtg gtg aaa tgt cca aag cat ttg tgc aag aat gtt   581
Tyr Cys Pro Ser Val Val Lys Cys Pro Lys His Leu Cys Lys Asn Val
        170                 175                 180

ggg ttg ttt gtg gat gag aaa ggg aac aag cgt ctt gct ctc act gat   629
Gly Leu Phe Val Asp Glu Lys Gly Asn Lys Arg Leu Ala Leu Thr Asp
    185                 190                 195

gtt ccc ctc aaa gtt caa ttc caa caa gcc taa acaagcttaa tgctcctcta 682
Val Pro Leu Lys Val Gln Phe Gln Gln Ala  *
200                 205
```

```
agtctaacat taatgcataa aaactatata tgaataagtg tatttccttt ctaataacga 742
tgcatgttct ttcaatgttt atcaggatcc tcatgtaagg ttttccttgg taaatgcaaa 802
ataaataaaa tgaacaaatg atataaaaaa aaaaaaaaaa aaaa              846
```

<210> 17
<211> 209
<212> PRT
<213> Glycine max

<400> 17

```
Met Lys Ser Thr Met Leu Leu Ala Phe Ala Leu Val Leu Ala Leu Ser
1               5                   10                  15
Ser Gln Pro Leu Leu Gly Gly Ala Glu Ala Ser Pro Glu Gln Val Val
            20                  25                  30
Asp Thr Leu Gly Lys Lys Leu Arg Val Gly Thr Asn Tyr Tyr Ile Val
        35                  40                  45
Pro Ser Leu Pro Tyr Thr Lys Ile Arg Thr Thr Arg Gly Leu Gly Leu
    50                  55                  60
Ala Ser Val Gly Lys Pro Tyr Cys Pro Leu Asp Val Val Val Val Asn
65                  70                  75                  80
```

18

```
Gly Tyr His Gly Leu Pro Val Thr Phe Ser Pro Val Asn Pro Lys Lys
                85                  90                  95
Gly Val Ile Arg Val Ser Thr Asp Leu Asn Ile Lys Phe Ser Ala Arg
            100                 105                 110
Thr Ser Cys Pro Arg Gln Tyr Ser Thr Val Trp Lys Leu Asp Asp Phe
            115                 120                 125
Asp Phe Ser Lys Arg Gln Trp Phe Val Thr Thr Gly Gly Val Val Gly
        130                 135                 140
Asn Pro Ser Leu Glu Thr Ile His Asn Trp Phe Lys Ile Glu Lys Tyr
145                 150                 155                 160
Asp Gly Ala Tyr Lys Leu Val Tyr Cys Pro Ser Val Val Lys Cys Pro
                165                 170                 175
Lys His Leu Cys Lys Asn Val Gly Leu Phe Val Asp Glu Lys Gly Asn
            180                 185                 190
Lys Arg Leu Ala Leu Thr Asp Val Pro Leu Lys Val Gln Phe Gln Gln
        195                 200                 205
Ala


<210> 18
<211> 1410
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (31)...(1095)

<400> 18
cggcacgaga agcaaacata acttgcagta atg gct tca atg aat aac caa aaa    54
                                   Met Ala Ser Met Asn Asn Gln Lys
                                    1                   5


gaa att gag ctc ttt gag ggc caa tct ctt ctg tac atg cag cta tat   102
Glu Ile Glu Leu Phe Glu Gly Gln Ser Leu Leu Tyr Met Gln Leu Tyr
     10                  15                  20


ggg cac cta aga cct atg tgt ctt aag tgg gct gtt caa cta ggt att   150
Gly His Leu Arg Pro Met Cys Leu Lys Trp Ala Val Gln Leu Gly Ile
 25                  30                  35                  40


cca gac ata ata cag aac cat gcc aaa ccc att tct ctt tct gac ttg   198
Pro Asp Ile Ile Gln Asn His Ala Lys Pro Ile Ser Leu Ser Asp Leu
                45                  50                  55


gtc tct act ctt caa att cca cca gct aac gct gct ttt gtg cag cgg   246
Val Ser Thr Leu Gln Ile Pro Pro Ala Asn Ala Ala Phe Val Gln Arg
            60                  65                  70


ttc atg cgc ttc ttg gca cac aat gga atc ttt gag atc cat gag agc   294
Phe Met Arg Phe Leu Ala His Asn Gly Ile Phe Glu Ile His Glu Ser
        75                  80                  85


caa gaa gat cat gaa cta aca tat gct cta acc cct gca tca aag ctt   342
Gln Glu Asp His Glu Leu Thr Tyr Ala Leu Thr Pro Ala Ser Lys Leu
    90                  95                  100
```

19

```
ctt gtc aat agt agt gat cat tgt cta tct cca atg gtt cta gcg ttt    390
Leu Val Asn Ser Ser Asp His Cys Leu Ser Pro Met Val Leu Ala Phe
105               110             115                 120

acc gat cca ctt cgg aac gtt aaa tac cat cac ttg ggg gaa tgg att    438
Thr Asp Pro Leu Arg Asn Val Lys Tyr His His Leu Gly Glu Trp Ile
                125             130                 135

cgt ggg gag gac ccc tca gta ttt gag aca gcc cac gga aca agc gct    486
Arg Gly Glu Asp Pro Ser Val Phe Glu Thr Ala His Gly Thr Ser Ala
                140             145                 150

tgg gga ctt ctt gag aaa aat cct gaa tat ttt agt ctc ttc aat gag    534
Trp Gly Leu Leu Glu Lys Asn Pro Glu Tyr Phe Ser Leu Phe Asn Glu
                155             160                 165

gct atg gca agt gat tcc cga ata gta gac ttg gca ctc aaa aat tgc    582
Ala Met Ala Ser Asp Ser Arg Ile Val Asp Leu Ala Leu Lys Asn Cys
        170             175                 180

act tca gtt ttt gag ggg cta gat tcc atg gtg gat gtt ggt ggt gga    630
Thr Ser Val Phe Glu Gly Leu Asp Ser Met Val Asp Val Gly Gly Gly
185             190                 195                 200

act gga acc acg gcc aga att atc tgt gac gca ttt cct aag ttg aaa    678
Thr Gly Thr Thr Ala Arg Ile Ile Cys Asp Ala Phe Pro Lys Leu Lys
                205             210                 215

tgt gtt gtg ctt gac ctt cct cat gtt gta gag aac ttg aca ggg acc    726
Cys Val Val Leu Asp Leu Pro His Val Val Glu Asn Leu Thr Gly Thr
                220             225                 230

aat aat ttg agt ttt gtt ggt ggt gac atg ttc aac tct atc cct caa    774
Asn Asn Leu Ser Phe Val Gly Gly Asp Met Phe Asn Ser Ile Pro Gln
                235             240                 245

gct gat gca gtg cta cta aag tgg gtt tta cat aat tgg acc gac gaa    822
Ala Asp Ala Val Leu Leu Lys Trp Val Leu His Asn Trp Thr Asp Glu
        250             255                 260

aat tgc ata aag atc ctg caa aag tgt aga gat tct att tca agc aaa    870
Asn Cys Ile Lys Ile Leu Gln Lys Cys Arg Asp Ser Ile Ser Ser Lys
265             270                 275                 280

ggc aac agt gga aaa gtg att atc ata gat gcc gta ata aat gag aag    918
Gly Asn Ser Gly Lys Val Ile Ile Ile Asp Ala Val Ile Asn Glu Lys
                285             290                 295

cta gat gac ccg gat atg aca caa aca aag ctt agt ttg gac att att    966
Leu Asp Asp Pro Asp Met Thr Gln Thr Lys Leu Ser Leu Asp Ile Ile
                300             305                 310

atg ttg acg atg aat gga aga gag aga acg gaa aaa gaa tgg aaa caa    1014
Met Leu Thr Met Asn Gly Arg Glu Arg Thr Glu Lys Glu Trp Lys Gln
                315             320                 325

ctc ttc atc gaa gca gga ttc aaa cac tac aaa ata ttt ccc atc ttt    1062
Leu Phe Ile Glu Ala Gly Phe Lys His Tyr Lys Ile Phe Pro Ile Phe
```
20

```
ggt ttt aga tct ctg att gag gtc tat cct tga acatttttat gatgtgtatg 1115
Gly Phe Arg Ser Leu Ile Glu Val Tyr Pro  *
345                     350

tcacacttaa cgtttatatt tatgaacatc ctcagacatc gttgtaattg tatttagtgg 1175
tttgcgtgtt gtttgctgaa taaagctatg atgacatagc attatcaact tctggtggaa 1235
ttacattatg ttcctccccg ctatgttgtt aaatgttctg tgtacggatt tctcattcct 1295
atttggccaa aataaattga ataaacatgt aatggatgca atcaatatac aatgttttgg 1355
tatggcttta cgtctttaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa        1410
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<210> 19
<211> 354
<212> PRT
<213> Glycine max

<400> 19
Met Ala Ser Met Asn Asn Gln Lys Glu Ile Glu Leu Phe Glu Gly Gln
 1   5   10   15
Ser Leu Leu Tyr Met Gln Leu Tyr Gly His Leu Arg Pro Met Cys Leu
            20   25   30
Lys Trp Ala Val Gln Leu Gly Ile Pro Asp Ile Ile Gln Asn His Ala
            35   40   45
Lys Pro Ile Ser Leu Ser Asp Leu Val Ser Thr Leu Gln Ile Pro Pro
    50   55   60
Ala Asn Ala Ala Phe Val Gln Arg Phe Met Arg Phe Leu Ala His Asn
65   70   75   80
Gly Ile Phe Glu Ile His Glu Ser Gln Glu Asp His Glu Leu Thr Tyr
                85   90   95
Ala Leu Thr Pro Ala Ser Lys Leu Leu Val Asn Ser Ser Asp His Cys
            100   105   110
Leu Ser Pro Met Val Leu Ala Phe Thr Asp Pro Leu Arg Asn Val Lys
            115   120   125
Tyr His His Leu Gly Glu Trp Ile Arg Gly Glu Asp Pro Ser Val Phe
    130   135   140
Glu Thr Ala His Gly Thr Ser Ala Trp Gly Leu Leu Glu Lys Asn Pro
145   150   155   160
Glu Tyr Phe Ser Leu Phe Asn Glu Ala Met Ala Ser Asp Ser Arg Ile
                165   170   175
Val Asp Leu Ala Leu Lys Asn Cys Thr Ser Val Phe Glu Gly Leu Asp
            180   185   190
Ser Met Val Asp Val Gly Gly Gly Thr Gly Thr Thr Ala Arg Ile Ile
            195   200   205
Cys Asp Ala Phe Pro Lys Leu Lys Cys Val Val Leu Asp Leu Pro His
    210   215   220
Val Val Glu Asn Leu Thr Gly Thr Asn Asn Leu Ser Phe Val Gly Gly
225   230   235   240
Asp Met Phe Asn Ser Ile Pro Gln Ala Asp Ala Val Leu Leu Lys Trp
                245   250   255
Val Leu His Asn Trp Thr Asp Glu Asn Cys Ile Lys Ile Leu Gln Lys
            260   265   270
Cys Arg Asp Ser Ile Ser Ser Lys Gly Asn Ser Gly Lys Val Ile Ile
            275   280   285
Ile Asp Ala Val Ile Asn Glu Lys Leu Asp Asp Pro Asp Met Thr Gln
    290   295   300
Thr Lys Leu Ser Leu Asp Ile Ile Met Leu Thr Met Asn Gly Arg Glu
305   310   315   320
```

21

```
Arg Thr Glu Lys Glu Trp Lys Gln Leu Phe Ile Glu Ala Gly Phe Lys
            325                     330                     335
His Tyr Lys Ile Phe Pro Ile Phe Gly Phe Arg Ser Leu Ile Glu Val
            340                     345                     350
Tyr Pro
```

<210> 20
<211> 1630
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (93)...(1403)

<400> 20

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cacctatagt actctcacct tctctcaatc attttttcatt catttgtcaa ctttttataga 60
cctcgattag tgtatgcaaa tttctttagg ac atg tgg cct aca tta gtg gct 113
                                   Met Trp Pro Thr Leu Val Ala
                                   1                   5

aat aag ata ttc aag aag aga ctt gga agc agc aat ttt ata gcg gat   161
Asn Lys Ile Phe Lys Lys Arg Leu Gly Ser Ser Asn Phe Ile Ala Asp
        10              15                  20

tat cct agt tat aaa gaa ccc ttg ctg ggt att gta gac att gat cag   209
Tyr Pro Ser Tyr Lys Glu Pro Leu Leu Gly Ile Val Asp Ile Asp Gln
    25              30                  35

aac tca aaa acc att ctt aat gat cac aag gac tca cac aaa tac aag   257
Asn Ser Lys Thr Ile Leu Asn Asp His Lys Asp Ser His Lys Tyr Lys
40              45                  50                  55

gta ttt gtt agt aca tgg aac gta ggt ggg att gca ccg gat gaa gat   305
Val Phe Val Ser Thr Trp Asn Val Gly Gly Ile Ala Pro Asp Glu Asp
                60                  65                  70

ttg aat ata gat gat ttg ttg gag aca tgc aac aac tct tgt gac atc   353
Leu Asn Ile Asp Asp Leu Leu Glu Thr Cys Asn Asn Ser Cys Asp Ile
                75                  80                  85

tat ata cta ggg ttt caa gaa ata gtg cct cta aaa gca tca aat gta   401
Tyr Ile Leu Gly Phe Gln Glu Ile Val Pro Leu Lys Ala Ser Asn Val
            90                  95                  100

ttg ggg tcc gaa aac aat gag att tct atg aaa tgg aat tcc ata atc   449
Leu Gly Ser Glu Asn Asn Glu Ile Ser Met Lys Trp Asn Ser Ile Ile
    105             110                 115

agg gaa gcc ttg aac aag aaa ata aca cat caa agg gac aaa gat gct   497
Arg Glu Ala Leu Asn Lys Lys Ile Thr His Gln Arg Asp Lys Asp Ala
120             125                 130                 135

aaa aaa cag gag cta aag aat aat ttt ccc aat aag aaa gaa aat cca   545
Lys Lys Gln Glu Leu Lys Asn Asn Phe Pro Asn Lys Lys Glu Asn Pro
            140                 145                 150
```

22

```
gct aag tgc tgt gat gcc cca cat gat ttc caa tgt atc att agc aag      593
Ala Lys Cys Cys Asp Ala Pro His Asp Phe Gln Cys Ile Ile Ser Lys
            155                 160                 165

caa atg gtt gga tta ttc ata tct gtg tgg att aga aga gat ctt tgt      641
Gln Met Val Gly Leu Phe Ile Ser Val Trp Ile Arg Arg Asp Leu Cys
            170                 175                 180

cca ttc att cgg cat cca agc gtg tca tgt gta ggt tgt ggg ata atg      689
Pro Phe Ile Arg His Pro Ser Val Ser Cys Val Gly Cys Gly Ile Met
        185                 190                 195

ggc tgc tta gga aac aag ggt tct ata tca gtg aga ttt cag tta cat      737
Gly Cys Leu Gly Asn Lys Gly Ser Ile Ser Val Arg Phe Gln Leu His
200                 205                 210                 215

gaa acc agc ttc tgc ttt gtg tgc agc cat cta gct tca ggg ggc aga      785
Glu Thr Ser Phe Cys Phe Val Cys Ser His Leu Ala Ser Gly Gly Arg
                220                 225                 230

gaa ggg gat gag aag cac agg aac tct aat gtt gct gaa att ttt tct      833
Glu Gly Asp Glu Lys His Arg Asn Ser Asn Val Ala Glu Ile Phe Ser
            235                 240     .           245

cgg aca agt ttt cct aga ggc cct ttg ctt gat ttg cct aga acc att      881
Arg Thr Ser Phe Pro Arg Gly Pro Leu Leu Asp Leu Pro Arg Thr Ile
            250                 255                 260

ctt gat cat gat cat gta ata ttg ctt gga gat cta aat tac aga att      929
Leu Asp His Asp His Val Ile Leu Leu Gly Asp Leu Asn Tyr Arg Ile
            265                 270                 275          .       .

tct cta cca gaa gaa acc aca cgc ttg ctt gtt gaa aaa aga gac tgg      977
Ser Leu Pro Glu Glu Thr Thr Arg Leu Leu Val Glu Lys Arg Asp Trp
280                 285                 290                 295

gat tct tta tta gca aat gat cag cta ata atg gag cta atg agt gga     1025
Asp Ser Leu Leu Ala Asn Asp Gln Leu Ile Met Glu Leu Met Ser Gly
            300                 305                 310

aac atg tta aga gga tgg cac gaa gga gca att aaa ttt gca cct acc     1073
Asn Met Leu Arg Gly Trp His Glu Gly Ala Ile Lys Phe Ala Pro Thr
            315                 320                 325

tac aaa tat tgt cca aat tca gac att tac tat gga tgc tgc tat cat     1121
Tyr Lys Tyr Cys Pro Asn Ser Asp Ile Tyr Tyr Gly Cys Cys Tyr His
            330                 335                 340

ggc aaa aag gca gaa aag aga aga gca cca gca tgg tgt gat cga ata     1169
Gly Lys Lys Ala Glu Lys Arg Arg Ala Pro Ala Trp Cys Asp Arg Ile
            345                 350                 355

gta tgg tgc ggt gag ggt cta aag caa ctt cag tac act aga att gaa     1217
Val Trp Cys Gly Glu Gly Leu Lys Gln Leu Gln Tyr Thr Arg Ile Glu
360                 365                 370                 375

tca aaa cta tca gat cat agg cct gtt aag gca atg ttt ata gca gaa     1265
```

23

```
Ser Lys Leu Ser Asp His Arg Pro Val Lys Ala Met Phe Ile Ala Glu
            380                 385                 390

gtc agg gtt tta cca gag ctg atg aaa aac ttg caa agc ttg ttc cta   1313
Val Arg Val Leu Pro Glu Leu Met Lys Asn Leu Gln Ser Leu Phe Leu
            395                 400                 405

tca gaa aga tac gag caa att aaa act ccc ttt gaa gtt tcc acc act   1361
Ser Glu Arg Tyr Glu Gln Ile Lys Thr Pro Phe Glu Val Ser Thr Thr
            410                 415                 420

gaa gat ttt gta aat aga aaa cga tca agc ttc cgg ttg tga           1403
Glu Asp Phe Val Asn Arg Lys Arg Ser Ser Phe Arg Leu  *
            425                 430                 435

attttttgtg tgattcaagc taggctttaa attgtgattg tgattaatgt tgcaatttta 1463
tcacaatctt ttgtggagaa aaatttgcat aaaaatgtga ttgatgtgac cgttattaca 1523
atcagggact tcaacaaccg tgacattgtc atcactgttg tggttgcaca tggttttttt 1583
ctataaaaaa aaaactgtga tatatgtaaa aaaaaaaaaa aaaaaaa              1630

<210> 21
<211> 436
<212> PRT
<213> Glycine max

<400> 21
Met Trp Pro Thr Leu Val Ala Asn Lys Ile Phe Lys Lys Arg Leu Gly
 1               5                  10                  15
Ser Ser Asn Phe Ile Ala Asp Tyr Pro Ser Tyr Lys Glu Pro Leu Leu
            20                  25                  30
Gly Ile Val Asp Ile Asp Gln Asn Ser Lys Thr Ile Leu Asn Asp His
            35                  40                  45
Lys Asp Ser His Lys Tyr Lys Val Phe Val Ser Thr Trp Asn Val Gly
    50                  55                  60
Gly Ile Ala Pro Asp Glu Asp Leu Asn Ile Asp Asp Leu Leu Glu Thr
65                  70                  75                  80
Cys Asn Asn Ser Cys Asp Ile Tyr Ile Leu Gly Phe Gln Glu Ile Val
            85                  90                  95
Pro Leu Lys Ala Ser Asn Val Leu Gly Ser Glu Asn Asn Glu Ile Ser
            100                 105                 110
Met Lys Trp Asn Ser Ile Ile Arg Glu Ala Leu Asn Lys Lys Ile Thr
            115                 120                 125
His Gln Arg Asp Lys Asp Ala Lys Lys Gln Glu Leu Lys Asn Asn Phe
    130                 135                 140
Pro Asn Lys Lys Glu Asn Pro Ala Lys Cys Cys Asp Ala Pro His Asp
145                 150                 155                 160
Phe Gln Cys Ile Ile Ser Lys Gln Met Val Gly Leu Phe Ile Ser Val
            165                 170                 175
Trp Ile Arg Arg Asp Leu Cys Pro Phe Ile Arg His Pro Ser Val Ser
            180                 185                 190
Cys Val Gly Cys Gly Ile Met Gly Cys Leu Gly Asn Lys Gly Ser Ile
            195                 200                 205
Ser Val Arg Phe Gln Leu His Glu Thr Ser Phe Cys Phe Val Cys Ser
            210                 215                 220
His Leu Ala Ser Gly Gly Arg Glu Gly Asp Glu Lys His Arg Asn Ser
225                 230                 235                 240
Asn Val Ala Glu Ile Phe Ser Arg Thr Ser Phe Pro Arg Gly Pro Leu
            245                 250                 255
```

24

```
Leu Asp Leu Pro Arg Thr Ile Leu Asp His Asp His Val Ile Leu Leu
        260                 265                 270
Gly Asp Leu Asn Tyr Arg Ile Ser Leu Pro Glu Glu Thr Thr Arg Leu
        275                 280                 285
Leu Val Glu Lys Arg Asp Trp Asp Ser Leu Leu Ala Asn Asp Gln Leu
        290                 295                 300
Ile Met Glu Leu Met Ser Gly Asn Met Leu Arg Gly Trp His Glu Gly
305                 310                 315                 320
Ala Ile Lys Phe Ala Pro Thr Tyr Lys Tyr Cys Pro Asn Ser Asp Ile
            325                 330                 335
Tyr Tyr Gly Cys Cys Tyr His Gly Lys Lys Ala Glu Lys Arg Arg Ala
            340                 345                 350
Pro Ala Trp Cys Asp Arg Ile Val Trp Cys Gly Glu Gly Leu Lys Gln
            355                 360                 365
Leu Gln Tyr Thr Arg Ile Glu Ser Lys Leu Ser Asp His Arg Pro Val
        370                 375                 380
Lys Ala Met Phe Ile Ala Glu Val Arg Val Leu Pro Glu Leu Met Lys
385                 390                 395                 400
Asn Leu Gln Ser Leu Phe Leu Ser Glu Arg Tyr Glu Gln Ile Lys Thr
            405                 410                 415
Pro Phe Glu Val Ser Thr Thr Glu Asp Phe Val Asn Arg Lys Arg Ser
            420                 425                 430
Ser Phe Arg Leu
        435


<210> 22
<211> 1600
<212> DNA
<213> Glycine max

<400> 22
agcaccatca tctctatcat tcggaatgca accaagctaa aagattacta caactaattg 60
cttttcctta tcacattttc tgacgtatag tgtgatttta tatatttta cataagagaa 120
ataatttcta caaaaaaaat gttcgataaa ataagtagag aacgtgtatt aataatttct 180
acataagaaa taaagaaata tattagatat aataagtgat gcaagaaaga tggacaaaaa 240
taattacgta aatatcattc tataaattta ttattcatta tataaatagc attaccattg 300
ttgaaacttg aaagtgggtc catcgtttac aactaaagaa agacacccta gcgtaaaata 360
ttcaaccatc gacgtctact tcaattaaca tgaagatgta gttccatctc aacggatttc 420
cgtctcaaat aaaattctta ataacgtgct actaaccatt ggaatctgca gaatatctcg 480
tttagttggg cacaatccct caaaagcgat gtattttttt aatggaaaca atgcatgcca 540
caagaacgtt tatatataca taattttact aaacaaatcg taatacaaaa ctttattatt 600
ataacgtgat ttgtcacttt ttgcttcaga aaaatacttt gtacaaaaca ttaagacaat 660
aacataagtt gccaatacca tacataaaac tctttaatga atcataatga tgaaaattga 720
gagatatttta gttccatgat aaagagtgtg tttgtgtggg aatttgacca aacgcaattg 780
ttgttccagt gaaaactttt ctcgcgtgtt tggccttttg tgtctcagaa agctaatttt 840
ctccatttaa cgtggtttgg acccattttc aaacgcactc acagtgagtc cgtttctgta 900
gaagtccttc cagcaggcca cccctccccc aaagaaaaat ttaagaaaca agaagagaaa 960
gaaaaaaga aaaagaaaaa acaagtcaca tatttttattc ttatgtcagc caaaaacttg 1020
actagctgta gatggggcaa taataactag ctattcatca catttcctag ctaattgcct 1080
gttttgttat ggaccacatt cccacttgca ctcatcttca gcaatttaaa ttaggtaata 1140
aacattaaga tatcctttaa aatctactca acaaacagaa gaattcaaat ctgcaagaag 1200
ggtagaccca tgttttatac tagctttctc tatctctctc ccactgggac ataaatgttc 1260
ctatatttca aaaaatatat atatgatatg atgagcaatg cagccaaagg tgcatcatct 1320
tttacgtcac atgaaagcct ttcctacctc ttcaagctgc acaagccttt ctctttccca 1380
gaatgatttt tttccatttc ttgttattat tactcctttt ggactttcta tataatgctt 1440
tctatatacg tttccaataa taccacgtac actactcatg tgccaggaaa aggagcagca 1500
gtgaccacct agcaatagta ctctcgcctt ctctcaatca tttttcattt gtcaactttt 1560
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25

atagacctcg atttgtgtat gcaaatttct ttaggacatg   1600

<210> 23
<211> 465
<212> PRT
<213> Zea mays

<400> 23
Met Glu Asp Val Arg Ala Thr Tyr Ser Met Gly Lys Glu Leu Gly Arg
1   5   10   15
Gly Gln Phe Gly Val Thr His Leu Cys Thr His Arg Thr Ser Gly Glu
                20   25   30
Lys Leu Ala Cys Lys Thr Ile Ala Lys Arg Lys Leu Ala Ala Arg Glu
            35   40   45
Asp Val Asp Asp Val Arg Arg Glu Val Gln Ile Met His His Leu Ser
        50   55   60
Gly Gln Pro Asn Val Val Gly Leu Arg Gly Ala Tyr Glu Asp Lys Gln
65   70   75   80
Ser Val His Leu Val Met Glu Leu Cys Ala Gly Gly Glu Leu Phe Asp
                85   90   95
Arg Ile Ile Ala Arg Gly Gln Tyr Thr Glu Arg Gly Ala Ala Glu Leu
                100   105   110
Leu Arg Ala Ile Val Gln Ile Val His Thr Cys His Ser Met Gly Val
        115   120   125
Met His Arg Asp Ile Lys Pro Glu Asn Phe Leu Leu Leu Ser Lys Asp
        130   135   140
Glu Asp Ala Pro Leu Lys Ala Thr Asp Phe Gly Leu Ser Val Phe Phe
145   150   155   160
Lys Glu Gly Glu Leu Leu Arg Asp Ile Val Gly Ser Ala Tyr Tyr Ile
                165   170   175
Ala Pro Glu Val Leu Lys Arg Lys Tyr Gly Pro Glu Ala Asp Ile Trp
                180   185   190
Ser Val Gly Val Met Leu Tyr Ile Phe Leu Ala Gly Val Pro Pro Phe
        195   200   205
Trp Ala Glu Asn Glu Asn Gly Ile Phe Thr Ala Ile Leu Arg Gly Gln
        210   215   220
Leu Asp Leu Ser Ser Glu Pro Trp Pro His Ile Ser Pro Gly Ala Lys
225   230   235   240
Asp Leu Val Lys Lys Met Leu Asn Ile Asn Pro Lys Glu Arg Leu Thr
                245   250   255
Ala Phe Gln Val Leu Asn His Pro Trp Ile Lys Glu Asp Gly Asp Ala
                260   265   270
Pro Asp Thr Pro Leu Asp Asn Val Val Leu Asp Arg Leu Lys Gln Phe
                275   280   285
Arg Ala Met Asn Gln Phe Lys Lys Ala Ala Leu Arg Ile Ile Ala Gly
        290   295   300
Cys Leu Ser Glu Glu Glu Ile Thr Gly Leu Lys Glu Met Phe Lys Asn
305   310   315   320
Ile Asp Lys Asp Asn Ser Gly Thr Ile Thr Leu Asp Glu Leu Lys His
                325   330   335
Gly Leu Ala Lys His Gly Pro Lys Leu Ser Asp Ser Glu Met Glu Lys
            340   345   350
Leu Met Glu Ala Ala Asp Ala Asp Gly Asn Gly Leu Ile Asp Tyr Asp
        355   360   365
Glu Phe Val Thr Ala Thr Val His Met Asn Lys Leu Asp Arg Glu Glu
        370   375   380
His Leu Tyr Thr Ala Phe Gln Tyr Phe Asp Lys Asp Asn Ser Gly Tyr
385   390   395   400
26

```
Ile Thr Lys Glu Glu Leu Glu His Ala Leu Lys Glu Gln Gly Leu Tyr
            405                     410                     415
Asp Ala Asp Lys Ile Lys Asp Ile Ile Ser Asp Ala Asp Ser Asp Asn
            420                     425                     430
Asp Gly Arg Ile Asp Tyr Ser Glu Phe Val Ala Met Met Arg Lys Gly
            435                     440                     445
Thr Ala Gly Ala Glu Pro Met Asn Ile Lys Lys Arg Arg Asp Ile Val
    450                     455                     460
Leu
465


<210> 24
<211> 490
<212> PRT
<213> Arabidopsis thaliana

<400> 24
Met Ala Asn Lys Pro Arg Thr Arg Trp Val Leu Pro Tyr Lys Thr Lys
 1               5                  10                  15
Asn Val Glu Asp Asn Tyr Phe Leu Gly Gln Val Leu Gly Gln Gly Gln
            20                  25                  30
Phe Gly Thr Thr Phe Leu Cys Thr His Lys Gln Thr Gly Gln Lys Leu
            35                  40                  45
Ala Cys Lys Ser Ile Pro Lys Arg Lys Leu Leu Cys Gln Glu Asp Tyr
    50                  55                  60
Asp Asp Val Leu Arg Glu Ile Gln Ile Met His His Leu Ser Glu Tyr
65                  70                  75                  80
Pro Asn Val Val Arg Ile Glu Ser Ala Tyr Glu Asp Thr Lys Asn Val
                85                  90                  95
His Leu Val Met Glu Leu Cys Glu Gly Gly Glu Leu Phe Asp Arg Ile
            100                 105                 110
Val Lys Arg Gly His Tyr Ser Glu Arg Glu Ala Ala Lys Leu Ile Lys
            115                 120                 125
Thr Ile Val Gly Val Val Glu Ala Cys His Ser Leu Gly Val Val His
    130                 135                 140
Arg Asp Leu Lys Pro Glu Asn Phe Leu Phe Ser Ser Ser Asp Glu Asp
145                 150                 155                 160
Ala Ser Leu Lys Ser Thr Asp Phe Gly Leu Ser Val Phe Cys Thr Pro
                165                 170                 175
Gly Glu Ala Phe Ser Glu Leu Val Gly Ser Ala Tyr Tyr Val Ala Pro
            180                 185                 190
Glu Val Leu His Lys His Tyr Gly Pro Glu Cys Asp Val Trp Ser Ala
            195                 200                 205
Gly Val Ile Leu Tyr Ile Leu Leu Cys Gly Phe Pro Pro Phe Trp Ala
    210                 215                 220
Glu Ser Glu Ile Gly Ile Phe Arg Lys Ile Leu Gln Gly Lys Leu Glu
225                 230                 235                 240
Phe Glu Ile Asn Pro Trp Pro Ser Ile Ser Glu Ser Ala Lys Asp Leu
                245                 250                 255
Ile Lys Lys Met Leu Glu Ser Asn Pro Lys Lys Arg Leu Thr Ala His
            260                 265                 270
Gln Val Leu Cys His Pro Trp Ile Val Asp Asp Lys Val Ala Pro Asp
            275                 280                 285
Lys Pro Leu Asp Cys Ala Val Val Ser Arg Leu Lys Lys Phe Ser Ala
    290                 295                 300
Met Asn Lys Leu Lys Lys Met Ala Leu Arg Val Ile Ala Glu Arg Leu
305                 310                 315                 320
```

27

```
Ser Glu Glu Glu Ile Gly Gly Leu Lys Glu Leu Phe Lys Met Ile Asp
            325             330             335
Thr Asp Lys Ser Gly Thr Ile Thr Phe Glu Glu Leu Lys Asp Ser Met
            340             345             350
Arg Arg Val Gly Ser Glu Leu Met Glu Ser Glu Ile Gln Glu Leu Leu
            355             360             365
Arg Ala Ala Asp Val Asp Glu Ser Gly Thr Ile Asp Tyr Gly Glu Phe
    370             375             380
Leu Ala Ala Thr Ile His Leu Asn Lys Leu Glu Arg Glu Glu Asn Leu
385             390             395             400
Val Ala Ala Phe Ser Phe Phe Asp Lys Asp Ala Ser Gly Tyr Ile Thr
            405             410             415
Ile Glu Glu Leu Gln Gln Ala Trp Lys Glu Phe Gly Ile Asn Asp Ser
            420             425             430
Asn Leu Asp Glu Met Ile Lys Asp Ile Asp Gln Asp Asn Asp Gly Gln
            435             440             445
Ile Asp Tyr Gly Glu Phe Val Ala Met Met Arg Lys Gly Asn Gly Thr
            450             455             460
Gly Gly Gly Ile Gly Arg Arg Thr Met Arg Asn Ser Leu Asn Phe Gly
465             470             475             480
Thr Thr Leu Pro Asp Glu Ser Met Asn Val
            485             490


<210> 25
<211> 205
<212> PRT
<213> Lycopersicon esculentum

<400> 25
Met Lys Ile Asn Gln Leu Phe Phe Pro Phe Leu Ile Leu Ala Ile Ser
 1               5               10              15
Phe Asn Ser Leu Leu Ser Ser Ala Ala Glu Ser Pro Pro Glu Val Val
            20              25              30
Asp Ile Asp Gly Lys Ile Leu Arg Thr Gly Val Asp Tyr Tyr Ile Leu
            35              40              45
Pro Val Val Arg Gly Arg Gly Gly Gly Leu Thr Met Asp Ser Ile Gly
    50              55              60
Asp Lys Met Cys Pro Leu Asp Ala Val Val Gln Glu His Asn Glu Ile
65              70              75              80
Asp Gln Gly Leu Pro Leu Thr Phe Thr Pro Val Asp Pro Lys Lys Gly
            85              90              95
Val Ile Arg Glu Ser Thr Asp Leu Asn Ile Ile Phe Ser Ala Asn Ser
            100             105             110
Ile Cys Val Gln Thr Thr Gln Trp Lys Leu Asp Asp Phe Asp Glu Thr
            115             120             125
Thr Gly Gln Tyr Phe Ile Thr Leu Gly Gly Asp Gln Gly Asn Pro Gly
            130             135             140
Val Glu Thr Ile Ser Asn Trp Phe Lys Ile Glu Lys Tyr Asp Arg Asp
145             150             155             160
Tyr Lys Leu Leu Tyr Cys Pro Thr Val Cys Asp Phe Cys Lys Val Ile
            165             170             175
Cys Arg Asp Ile Gly Ile Phe Ile Gln Asp Gly Val Arg Arg Leu Ala
            180             185             190
Leu Ser Asp Val Pro Phe Lys Val Met Phe Lys Lys Ala
            195             200             205
```

28

<210> 26
<211> 210
<212> PRT
<213> Nicotiana tabacum

<400> 26
Met Lys Thr Asn Gln Leu Phe Leu Pro Phe Leu Ile Phe Thr Ile Ser
1   5   10   15
Phe Asn Ser Phe Leu Ser Ser Ser Ala Glu Ala Pro Pro Ala Val Val
            20   25   30
Asp Ile Ala Gly Lys Lys Leu Arg Thr Gly Ile Asp Tyr Tyr Ile Leu
            35   40   45
Pro Val Val Arg Gly Arg Gly Gly Leu Thr Leu Asp Ser Thr Gly
    50   55   60
Asn Glu Ser Cys Pro Leu Asp Ala Val Val Gln Glu Gln Gln Glu Ile
65   70   75   80
Lys Asn Gly Leu Pro Leu Thr Phe Thr Pro Val Asn Pro Lys Lys Gly
                85   90   95
Val Ile Arg Glu Ser Thr Asp Leu Asn Ile Lys Phe Ser Ala Ala Ser
            100   105   110
Ile Cys Val Gln Thr Thr Leu Trp Lys Leu Asp Asp Phe Asp Glu Thr
            115   120   125
Thr Gly Lys Tyr Phe Ile Thr Ile Gly Gly Asn Glu Gly Asn Pro Gly
    130   135   140
Arg Glu Thr Ile Ser Asn Trp Phe Lys Ile Glu Lys Phe Glu Arg Asp
145   150   155   160
Tyr Lys Leu Val Tyr Cys Pro Thr Val Cys Asn Phe Cys Lys Val Ile
                165   170   175
Cys Lys Asp Val Gly Ile Phe Ile Gln Asp Gly Ile Arg Arg Leu Ala
            180   185   190
Leu Ser Asp Val Pro Phe Lys Val Met Phe Lys Lys Ala Gln Val Val
    195   200   205
Lys Asp
    210

<210> 27
<211> 364
<212> PRT
<213> Zea mays

<400> 27
Met Glu Leu Ser Pro Asn Asn Ser Thr Asp Gln Ser Leu Leu Asp Ala
1   5   10   15
Gln Leu Glu Leu Trp His Thr Thr Phe Ala Phe Met Lys Ser Met Ala
            20   25   30
Leu Lys Ser Ala Ile His Leu Arg Ile Ala Asp Ala Ile His Leu His
            35   40   45
Gly Gly Ala Ala Ser Leu Ser Gln Ile Leu Ser Lys Val His Leu His
    50   55   60
Pro Ser Arg Val Ser Ser Leu Arg Arg Leu Met Arg Val Leu Thr Thr
65   70   75   80
Thr Asn Val Phe Gly Thr Gln Pro Leu Gly Gly Gly Ser Asp Asp Asp
                85   90   95
Ser Glu Pro Val Tyr Thr Leu Thr Pro Val Ser Arg Leu Leu Ile Gly
            100   105   110
Ser Gln Ser Ser Gln Leu Ala Gln Thr Pro Leu Ala Ala Met Val Leu
    115   120   125

29

```
Asp Pro Thr Ile Val Ser Pro Phe Ser Glu Leu Gly Ala Trp Phe Gln
    130                 135                 140
His Glu Leu Pro Asp Pro Cys Ile Phe Lys His Thr His Gly Arg Gly
145                 150                 155                 160
Ile Trp Glu Leu Thr Lys Asp Asp Ala Thr Phe Asp Ala Leu Val Asn
                165                 170                 175
Asp Gly Leu Ala Ser Asp Ser Gln Leu Ile Val Asp Val Ala Ile Lys
            180                 185                 190
Gln Ser Ala Glu Val Phe Gln Gly Ile Ser Ser Leu Val Asp Val Gly
            195                 200                 205
Gly Gly Ile Gly Ala Ala Ala Gln Ala Ile Ser Lys Ala Phe Pro His
    210                 215                 220
Val Lys Cys Ser Val Leu Asp Leu Ala His Val Val Ala Lys Ala Pro
225                 230                 235                 240
Thr His Thr Asp Val Gln Phe Ile Ala Gly Asp Met Phe Glu Ser Ile
                245                 250                 255
Pro Pro Ala Asp Ala Val Leu Leu Lys Ser Val Leu His Asp Trp Asp
            260                 265                 270
His Asp Asp Cys Val Lys Ile Leu Lys Asn Cys Lys Lys Ala Ile Pro
    275                 280                 285
Pro Arg Glu Ala Gly Gly Lys Val Ile Ile Ile Asn Met Val Val Gly
    290                 295                 300
Ala Gly Pro Ser Asp Met Lys His Lys Glu Met Gln Ala Ile Phe Asp
305                 310                 315                 320
Val Tyr Ile Met Phe Ile Asn Gly Met Glu Arg Asp Glu Gln Glu Trp
                325                 330                 335
Ser Lys Ile Phe Ser Glu Ala Gly Tyr Ser Asp Tyr Arg Ile Ile Pro
            340                 345                 350
Val Leu Gly Val Arg Ser Ile Ile Glu Val Tyr Pro
            355                 360


<210> 28
<211> 352
<212> PRT
<213> Medicago sativa

<400> 28
Met Ala Ser Ser Ile Asn Gly Arg Lys Pro Ser Glu Ile Phe Lys Ala
1               5                   10                  15
Gln Ala Leu Leu Tyr Lys His Ile Tyr Ala Phe Ile Asp Ser Met Ser
            20                  25                  30
Leu Lys Trp Ala Val Glu Met Asn Ile Pro Asn Ile Ile Gln Asn His
            35                  40                  45
Gly Lys Pro Ile Ser Leu Ser Asn Leu Val Ser Ile Leu Gln Val Pro
    50                  55                  60
Ser Ser Lys Ile Gly Asn Val Arg Arg Leu Met Arg Tyr Leu Ala His
65                  70                  75                  80
Asn Gly Phe Phe Glu Ile Ile Thr Lys Glu Glu Glu Ser Tyr Ala Leu
                85                  90                  95
Thr Val Ala Ser Glu Leu Leu Val Arg Gly Ser Asp Leu Cys Leu Ala
            100                 105                 110
Pro Met Val Glu Cys Val Leu Asp Pro Thr Leu Ser Gly Ser Tyr His
            115                 120                 125
Glu Leu Lys Lys Trp Ile Tyr Glu Glu Asp Leu Thr Leu Phe Gly Val
    130                 135                 140
Thr Leu Gly Ser Gly Phe Trp Asp Phe Leu Asp Lys Asn Pro Glu Tyr
145                 150                 155                 160
```
30

```
Asn Thr Ser Phe Asn Asp Ala Met Ala Ser Asp Ser Lys Leu Ile Asn
                165                 170                 175
Leu Ala Leu Arg Asp Cys Asp Phe Val Phe Asp Gly Leu Glu Ser Ile
                180                 185                 190
Val Asp Val Gly Gly Gly Thr Gly Thr Thr Ala Lys Ile Ile Cys Glu
                195                 200                 205
Thr Phe Pro Lys Leu Lys Cys Ile Val Phe Asp Arg Pro Gln Val Val
    210                 215                 220
Glu Asn Leu Ser Gly Ser Asn Asn Leu Thr Tyr Val Gly Gly Asp Met
225                 230                 235                 240
Phe Thr Ser Ile Pro Asn Ala Asp Ala Val Leu Leu Lys Tyr Ile Leu
                245                 250                 255
His Asn Trp Thr Asp Lys Asp Cys Leu Arg Ile Leu Lys Lys Cys Lys
                260                 265                 270
Glu Ala Val Thr Asn Asp Gly Lys Arg Gly Lys Val Thr Ile Ile Asp
                275                 280                 285
Met Val Ile Asp Glu Lys Lys Asp Glu Asn Gln Val Thr Gln Ile Lys
    290                 295                 300
Leu Leu Met Asp Val Asn Met Ala Cys Leu Asn Gly Lys Glu Arg Asn
305                 310                 315                 320
Glu Glu Glu Trp Lys Lys Leu Phe Ile Glu Ala Gly Phe Gln His Tyr
                325                 330                 335
Lys Ile Ser Pro Leu Thr Gly Phe Leu Ser Leu Ile Glu Ile Tyr Pro
                340                 345                 350


<210> 29
<211> 664
<212> PRT
<213> Arabidopsis thaliana

<400> 29
Met Ser Pro Val Glu Pro Ala Gly Ile Met Lys Lys Ser His Arg Gln
  1               5                  10                  15
Lys Ser Gln Arg Leu Trp Ala Lys Leu Val Met Arg Lys Trp Leu Asn
                20                  25                  30
Ile Ser Gly Arg Asp Pro Glu Tyr Gly Ala Asp Thr Asp Asn Glu Ser
                35                  40                  45
Glu Asn Glu Asp Ala Arg Glu Asp Asn Asp Asp Ser Ser Ser Asp Glu
    50                  55                  60
Glu Gly Gly Ser Gly Ser Arg Gly Arg Glu Ser Lys Val Tyr Glu Asn
65                  70                  75                  80
Ala Glu Asp Ala Ile Ala Ala Ala Ser Ala Val Val Asp Ala Ala Ala
                85                  90                  95
Ala Ala Ala Glu Phe Ile Ser Asn Asp Ala Pro Met Lys Leu Arg Arg
                100                 105                 110
Arg Asn Ser Glu Thr Leu Arg Ala Gln Tyr Ile Asn Asn Lys Glu Ile
                115                 120                 125
Arg Val Cys Val Gly Thr Trp Asn Val Gly Gly Ile Ser Pro Pro Ser
    130                 135                 140
Asp Leu Asp Ile Asp Asp Trp Ile Glu Ile Asn Gln Pro Ala Asp Ile
145                 150                 155                 160
Tyr Val Leu Gly Ser Gln Glu Ile Val Pro Leu Asn Ala Gly Asn Ile
                165                 170                 175
Leu Gly Ala Glu Asp Asp Arg Pro Val Ala Lys Trp Glu Glu Val Ile
                180                 185                 190
Arg Glu Ala Leu Asn Arg Val Arg Pro Lys Leu Ser Gly Val Lys Ser
                195                 200                 205
```

31

```
Tyr Ser Asp Pro Pro Ser Pro Gly Arg Phe Lys Pro Phe Glu Glu Thr
    210             215             220
His Asp Ile Ile Glu Glu Glu Val Ala Phe Glu Ser Asp Ser Asp Ala
225             230             235             240
Gly Val Glu Ile His Pro Ile Asp Glu Glu Glu Glu Glu Glu Thr Asp
            245             250             255
Arg Leu Trp Ala Leu Lys His Asp Gly Gly Val Ile Gly Glu Val Lys
            260             265             270
Thr Leu Val Asp Pro Asn Thr Gly Leu Pro Val Val Glu Ile Lys Arg
        275             280             285
Gln Phe Ser Ile Pro Lys Lys Leu Asp Arg Gln Leu Cys Leu Arg Ala
    290             295             300
Asp Ser Phe Lys Gly Ile Ser Asp Asp Asp Ser Thr Gln Thr Gly Met
305             310             315             320
Lys Thr Ile Asn Arg Met Leu Ser Gly Lys Glu Arg Ile Gly Leu Ser
            325             330             335
Trp Pro Glu Pro Pro Leu Asn Met Leu Gly Pro Cys Val Leu Asp Arg
            340             345             350
Gln Pro Ser Ile Lys Thr Val Lys Ser Leu Lys Thr Ala Lys Ser Phe
        355             360             365
Lys Ala Tyr Ser Ser Phe Lys Ser Val Ala Gly Asn Asn Asn Gly Ile
    370             375             380
Pro Pro Glu Val Leu Ala Leu Ala Glu Met Asp Leu Lys Leu Leu Met
385             390             395             400
Glu Arg Lys Arg Arg Pro Ala Tyr Val Arg Leu Val Ser Lys Gln Met
            405             410             415
Val Gly Ile Leu Leu Thr Ile Trp Val Lys Arg Ser Leu Arg Lys His
            420             425             430
Ile Gln Asn Val Arg Val Ser Thr Val Gly Val Gly Val Met Gly Tyr
        435             440             445
Ile Gly Asn Lys Gly Ala Val Ser Val Ser Met Ser Ile Asn Gln Thr
    450             455             460
Phe Phe Cys Phe Ile Asn Thr His Leu Thr Ala Gly Glu Arg Glu Val
465             470             475             480
Asp Gln Ile Lys Arg Asn Ala Asp Val His Glu Ile His Lys Arg Thr
            485             490             495
Val Phe His Ser Val Ser Ala Leu Gly Leu Pro Lys Leu Ile Tyr Asp
            500             505             510
His Glu Arg Ile Ile Trp Leu Gly Asp Leu Asn Tyr Arg Leu Ser Ser
            515             520             525
Ser Tyr Glu Lys Thr Arg Asp Leu Ile Ser Lys Arg Glu Trp Ser Lys
    530             535             540
Leu Leu Glu Tyr Asp Gln Leu Val Lys Glu Tyr Arg Lys Gly Arg Ala
545             550             555             560
Phe Asp Gly Trp Ser Glu Gly Thr Leu His Phe Pro Pro Thr Tyr Lys
            565             570             575
Tyr Gln Ala Asn Ser Asp Glu Tyr Thr Ala Asn Asp Gly Lys Ala Pro
        580             585             590
Lys Arg Thr Pro Ala Trp Cys Asp Arg Val Leu Ser Tyr Gly Lys Gly
        595             600             605
Met Arg Leu Val His Tyr Arg Arg Thr Glu Gln Lys Phe Ser Asp His
    610             615             620
Arg Pro Val Thr Ala Ile Tyr Met Ala Glu Val Glu Val Phe Ser Ala
625             630             635             640
Arg Lys Leu Gln Arg Ala Leu Thr Phe Thr Asp Ala Glu Ile Glu Asp
            645             650             655
Glu Gly Leu Val Ala Val Leu Val
            660
```

32

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<210> 30
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> cAMP and cGMP-dependent protein phosphorylation
      site

<221> DOMAIN
<222> (1)...(4)
<223> cAMP and cGMP-dependent protein phosphorylation
      site

<400> 30
Arg Lys Arg Ser
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<210> 31
<211> 246
<212> PRT
<213> Arabidopsis thaliana

<400> 31
Met Cys Gly Gly Ala Ile Ile Ser Asp Tyr Ala Pro Leu Val Thr Lys
 1               5                  10                  15
Ala Lys Gly Arg Lys Leu Thr Ala Glu Glu Leu Trp Ser Glu Leu Asp
                20                  25                  30
Ala Ser Ala Ala Asp Asp Phe Trp Gly Phe Tyr Ser Thr Ser Lys Leu
                35                  40                  45
His Pro Thr Asn Gln Val Asn Val Lys Glu Glu Ala Val Lys Lys
        50                  55                  60
Glu Gln Ala Thr Glu Pro Gly Lys Arg Arg Lys Arg Lys Asn Val Tyr
65                  70                  75                  80
Arg Gly Ile Arg Lys Arg Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg
                85                  90                  95
Asp Pro Arg Lys Gly Val Arg Val Trp Leu Gly Thr Phe Asn Thr Ala
                100                 105                 110
Glu Glu Ala Ala Met Ala Tyr Asp Val Ala Ala Lys Gln Ile Arg Gly
                115                 120                 125
Glu Lys Ala Lys Leu Asn Phe Pro Asp Leu Asp His His Pro Ser Thr
                130                 135                 140
Pro Pro Pro Ser Ser Thr Ser Leu Arg Leu Ser Asp Gln Pro Pro Ala
145                 150                 155                 160
Lys Lys Val Cys Val Val Ser Gln Ser Glu Leu Ala Gln Pro Ser Phe
                165                 170                 175
Pro Val Glu Cys Val Gly Phe Gly Lys Gly Glu Glu Phe Gln Asn Leu
                180                 185                 190
Met Tyr Gly Phe Glu Pro Asp Tyr Asp Leu Lys Gln Gln Ile Ser Ser
                195                 200                 205
Leu Glu Ser Phe Leu Glu Leu Asp Gly Thr Thr Ala Glu Gln Pro Ser
                210                 215                 220
Gln Leu Asp Glu Ser Val Cys Asp Val Asp Met Trp Met Leu Asp Asp
225                 230                 235                 240
Val Ile Ala Ser Tyr Glu
```

33

<210> 32
<211> 248
<212> PRT
<213> Arabidopsis thaliana

<400> 32
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Met Cys Gly Gly Ala Ile Ile Ser Asp Tyr Ala Pro Leu Val Thr Lys
 1               5                  10                  15
Ala Lys Gly Arg Lys Leu Thr Ala Glu Glu Leu Trp Ser Glu Leu Asp
                20                  25                  30
Ala Ser Ala Ala Asp Asp Phe Trp Gly Phe Tyr Ser Thr Ser Lys Leu
                35                  40                  45
His Pro Thr Asn Gln Val Asn Val Lys Glu Glu Ala Val Lys Lys Glu
        50                  55                  60
Gln Ala Thr Glu Pro Gly Lys Arg Arg Lys Arg Lys Asn Val Tyr Arg
65                  70                  75                  80
Gly Ile Arg Lys Arg Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp
                85                  90                  95
Pro Arg Lys Gly Val Arg Val Trp Leu Gly Thr Phe Asn Thr Ala Glu
                100                 105                 110
Glu Ala Ala Met Ala Tyr Asp Val Ala Ala Lys Gln Ile Arg Gly Asp
        115                 120                 125
Lys Ala Lys Leu Asn Phe Pro Asp Leu His His Pro Pro Pro Pro Asn
        130                 135                 140
Tyr Thr Pro Pro Pro Ser Ser Pro Arg Ser Thr Asp Gln Pro Pro Ala
145                 150                 155                 160
Lys Lys Val Cys Val Val Ser Gln Ser Glu Ser Glu Leu Ser Gln Pro
                165                 170                 175
Ser Phe Pro Val Glu Cys Ile Gly Phe Gly Asn Gly Asp Glu Phe Gln
                180                 185                 190
Asn Leu Ser Tyr Gly Phe Glu Pro Asp Tyr Asp Leu Lys Gln Gln Ile
        195                 200                 205
Ser Ser Leu Glu Ser Phe Leu Glu Leu Asp Gly Asn Thr Ala Glu Gln
        210                 215                 220
Pro Ser Gln Leu Asp Glu Ser Val Ser Glu Val Asp Met Trp Met Leu
225                 230                 235                 240
Asp Asp Val Ile Ala Ser Tyr Glu
                245
```

<210> 33
<211> 1908
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (24)...(1454)

<400> 33
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gcacgagatt caatcttcat ttg atg cta aat gcg gat aga gaa ttt ctt gct   53
                        Met Leu Asn Ala Asp Arg Glu Phe Leu Ala
                         1               5                   10

cag aag agt gct cca cat cga gac ttc tat aat gtt aga aaa gtt gat   101
```

```
Gln Lys Ser Ala Pro His Arg Asp Phe Tyr Asn Val Arg Lys Val Asp    .
                15                  20                  25

act cat gtc cac cac tca gca tgc atg aat cag aaa cat ctt tta agg   149
Thr His Val His His Ser Ala Cys Met Asn Gln Lys His Leu Leu Arg
            30                  35                  40

ttc ata aag tca aag ctg aga aaa gag cct gat gag gtt gta ata ttt   197
Phe Ile Lys Ser Lys Leu Arg Lys Glu Pro Asp Glu Val Val Ile Phe
            45                  50                  55

cga gat ggg aca tat cta acg ttg gaa gag gtt ttc aag agt tta gat   245
Arg Asp Gly Thr Tyr Leu Thr Leu Glu Glu Val Phe Lys Ser Leu Asp
        60                  65                  70

ttg tct gga tat gac ctc aat gtt gac ctt ttg gac gtt cac gca gac   293
Leu Ser Gly Tyr Asp Leu Asn Val Asp Leu Leu Asp Val His Ala Asp
    75                  80                  85                  90

aag agt act ttt cat cgc ttt gat aag ttc aat ctt aaa tac aat cct   341
Lys Ser Thr Phe His Arg Phe Asp Lys Phe Asn Leu Lys Tyr Asn Pro
                95                  100                 105

tgc ggt caa agt agg ctc agg gag ata ttt ctt aag cag gat aat ctc   389
Cys Gly Gln Ser Arg Leu Arg Glu Ile Phe Leu Lys Gln Asp Asn Leu
            110                 115                 120

att caa ggt cgt ttt ctt ggt gag tta act aag caa gtg ttt tca gat   437
Ile Gln Gly Arg Phe Leu Gly Glu Leu Thr Lys Gln Val Phe Ser Asp
            125                 130                 135

ctt gct gcc agt aaa tat cag atg gct gaa tat aga ata tca ata tat   485
Leu Ala Ala Ser Lys Tyr Gln Met Ala Glu Tyr Arg Ile Ser Ile Tyr
        140                 145                 150

ggt agg aag caa agt gag tgg gac caa cta gcc agt tgg ata gtg aat   533
Gly Arg Lys Gln Ser Glu Trp Asp Gln Leu Ala Ser Trp Ile Val Asn
155                 160                 165                 170

aat gat ttg tac agc gag aat gtc gtt tgg ttg att cag ctt cca cgg   581
Asn Asp Leu Tyr Ser Glu Asn Val Val Trp Leu Ile Gln Leu Pro Arg
                175                 180                 185

ttg tac aat gtg tac aaa gaa atg gga att gtg aca tca ttc cag aac   629
Leu Tyr Asn Val Tyr Lys Glu Met Gly Ile Val Thr Ser Phe Gln Asn
            190                 195                 200

atg ctc gac aat att ttc att cca ctt ttt gag gtc act gtc aac cca   677
Met Leu Asp Asn Ile Phe Ile Pro Leu Phe Glu Val Thr Val Asn Pro
            205                 210                 215

gat tca cat cct cag ctg cat gtt ttc ctg aaa cag gtt gtt ggg ttg   725
Asp Ser His Pro Gln Leu His Val Phe Leu Lys Gln Val Val Gly Leu
        220                 225                 230

gat ttg gtt gat gat gaa agc aaa cct gaa aga cgg cca aca aaa cac   773
Asp Leu Val Asp Asp Glu Ser Lys Pro Glu Arg Arg Pro Thr Lys His
235                 240                 245                 250
```

35

```
atg cct aca cct gag caa tgg act aat gtt ttc aat ccg gca ttt tca      821
Met Pro Thr Pro Glu Gln Trp Thr Asn Val Phe Asn Pro Ala Phe Ser
            255             260             265

tac tat gtc tat tac tgt tat gca aat ctt tac acc tta aac aag ctt      869
Tyr Tyr Val Tyr Tyr Cys Tyr Ala Asn Leu Tyr Thr Leu Asn Lys Leu
            270             275             280

cga gaa tca aag gga atg aca aca atc aaa ttc cgt cca cat tct gga      917
Arg Glu Ser Lys Gly Met Thr Thr Ile Lys Phe Arg Pro His Ser Gly
            285             290             295

gag gct ggt gat att gac cac ctt gca gca acc ttt ctc acg gct cac      965
Glu Ala Gly Asp Ile Asp His Leu Ala Ala Thr Phe Leu Thr Ala His
            300             305             310

aac att gca cat gga atc aat ttg aaa aaa tct cct gtg ctt caa tat     1013
Asn Ile Ala His Gly Ile Asn Leu Lys Lys Ser Pro Val Leu Gln Tyr
315             320             325             330

tta tat tat tta gcc cag att ggg ctg gca atg tct cct ttg agc aat     1061
Leu Tyr Tyr Leu Ala Gln Ile Gly Leu Ala Met Ser Pro Leu Ser Asn
            335             340             345

aac tcc cta ttc tta gac tac cat cgg aat cct ttt cca atg ttc ttc     1109
Asn Ser Leu Phe Leu Asp Tyr His Arg Asn Pro Phe Pro Met Phe Phe
            350             355             360

tta cgg ggt ctg aat gtg tca ctt tct act gat gat cct ctc caa att     1157
Leu Arg Gly Leu Asn Val Ser Leu Ser Thr Asp Asp Pro Leu Gln Ile
            365             370             375

cac tta aca aag gaa cca ttg gtt gaa gaa tat agc ata gct gct tct     1205
His Leu Thr Lys Glu Pro Leu Val Glu Glu Tyr Ser Ile Ala Ala Ser
            380             385             390

gtg tgg aag ttg agc tca tgt gat tta tgt gag att gcc cgt aat tca     1253
Val Trp Lys Leu Ser Ser Cys Asp Leu Cys Glu Ile Ala Arg Asn Ser
395             400             405             410

gtt tat caa tca ggt ttc tca cat gct tta aag tca cat tgg att ggt     1301
Val Tyr Gln Ser Gly Phe Ser His Ala Leu Lys Ser His Trp Ile Gly
            415             420             425

aag gag tac tac aag agt ggg cca cgc gga aat gac att cag aga aca     1349
Lys Glu Tyr Tyr Lys Ser Gly Pro Arg Gly Asn Asp Ile Gln Arg Thr
            430             435             440

aac gtt cct cac atc cgg ttg gaa ttc cgt gat acg att tgg aga gag     1397
Asn Val Pro His Ile Arg Leu Glu Phe Arg Asp Thr Ile Trp Arg Glu
            445             450             455

gag atg caa cag gtt tat ttg ggc aaa gcc atc att cct gaa gta gta     1445
Glu Met Gln Gln Val Tyr Leu Gly Lys Ala Ile Ile Pro Glu Val Val
            460             465             470

gac aaa taa gatgccaggg ggcattcctt tcatacacat gaggtagata            1494
Asp Lys
```
36

```
Asp Lys   *
475
```

```
gtatcctcaa accccttgcag cgtcagagat gcagggctga agacatacaa tgctggtctg 1554
atgatatgag ccaggtacat actatagaga atcaacaaga tcgatgagct tgagcatcga 1614
acaaggtttt acagctacaa atcgacgtac ccgtggggtt ttttctatcc ttgggttaga 1674
gttaaaatta ttagggttag caattagttc atgcttcaag caaaatgatg cctgtcggtg 1734
ttagaaatgt atgttagtaa tgtaagttat gatcctttga agggagagag atattcatct 1794
cccaaaattt tgattcccat tgtttatcga taataatata tcgtgaacga cagttgagac 1854
ttgaaaaacg gtggctctat tagttttacc gtaaaaaaaa aaaaaaaaa aaaa      1908
```

```
<210> 34
<211> 476
<212> PRT
<213> Glycine max
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```
<400> 34
Met Leu Asn Ala Asp Arg Glu Phe Leu Ala Gln Lys Ser Ala Pro His
 1               5                  10                  15
Arg Asp Phe Tyr Asn Val Arg Lys Val Asp Thr His Val His His Ser
             20                  25                  30
Ala Cys Met Asn Gln Lys His Leu Leu Arg Phe Ile Lys Ser Lys Leu
         35                  40                  45
Arg Lys Glu Pro Asp Glu Val Val Ile Phe Arg Asp Gly Thr Tyr Leu
     50                  55                  60
Thr Leu Glu Glu Val Phe Lys Ser Leu Asp Leu Ser Gly Tyr Asp Leu
65                  70                  75                  80
Asn Val Asp Leu Leu Asp Val His Ala Asp Lys Ser Thr Phe His Arg
                 85                  90                  95
Phe Asp Lys Phe Asn Leu Lys Tyr Asn Pro Cys Gly Gln Ser Arg Leu
            100                 105                 110
Arg Glu Ile Phe Leu Lys Gln Asp Asn Leu Ile Gln Gly Arg Phe Leu
         115                 120                 125
Gly Glu Leu Thr Lys Gln Val Phe Ser Asp Leu Ala Ala Ser Lys Tyr
     130                 135                 140
Gln Met Ala Glu Tyr Arg Ile Ser Ile Tyr Gly Arg Lys Gln Ser Glu
145                 150                 155                 160
Trp Asp Gln Leu Ala Ser Trp Ile Val Asn Asn Asp Leu Tyr Ser Glu
            165                 170                 175
Asn Val Val Trp Leu Ile Gln Leu Pro Arg Leu Tyr Asn Val Tyr Lys
            180                 185                 190
Glu Met Gly Ile Val Thr Ser Phe Gln Asn Met Leu Asp Asn Ile Phe
     195                 200                 205
Ile Pro Leu Phe Glu Val Thr Val Asn Pro Asp Ser His Pro Gln Leu
     210                 215                 220
His Val Phe Leu Lys Gln Val Val Gly Leu Asp Leu Val Asp Asp Glu
225                 230                 235                 240
Ser Lys Pro Glu Arg Arg Pro Thr Lys His Met Pro Thr Pro Glu Gln
            245                 250                 255
Trp Thr Asn Val Phe Asn Pro Ala Phe Ser Tyr Tyr Val Tyr Tyr Cys
            260                 265                 270
Tyr Ala Asn Leu Tyr Thr Leu Asn Lys Leu Arg Glu Ser Lys Gly Met
         275                 280                 285
Thr Thr Ile Lys Phe Arg Pro His Ser Gly Glu Ala Gly Asp Ile Asp
         290                 295                 300
His Leu Ala Ala Thr Phe Leu Thr Ala His Asn Ile Ala His Gly Ile
305                 310                 315                 320
Asn Leu Lys Lys Ser Pro Val Leu Gln Tyr Leu Tyr Tyr Leu Ala Gln
```

```
                     325                      330                      335
Ile Gly Leu Ala Met Ser Pro Leu Ser Asn Asn Ser Leu Phe Leu Asp
                 340                  345                  350
Tyr His Arg Asn Pro Phe Pro Met Phe Phe Leu Arg Gly Leu Asn Val
             355                  360                  365
Ser Leu Ser Thr Asp Asp Pro Leu Gln Ile His Leu Thr Lys Glu Pro
         370                  375                  380
Leu Val Glu Glu Tyr Ser Ile Ala Ala Ser Val Trp Lys Leu Ser Ser
385                  390                  395                  400
Cys Asp Leu Cys Glu Ile Ala Arg Asn Ser Val Tyr Gln Ser Gly Phe
             405                  410                  415
Ser His Ala Leu Lys Ser His Trp Ile Gly Lys Glu Tyr Tyr Lys Ser
         420                  425                  430
Gly Pro Arg Gly Asn Asp Ile Gln Arg Thr Asn Val Pro His Ile Arg
         435                  440                  445
Leu Glu Phe Arg Asp Thr Ile Trp Arg Glu Glu Met Gln Gln Val Tyr
     450                  455                  460
Leu Gly Lys Ala Ile Ile Pro Glu Val Val Asp Lys
465                  470                  475
```